

Title: GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 23, 2002, 11:08:56 ; Search time 29.56 Seconds
(without alignments)
172.848 Million cell updates/sec

Title: US-09-813-383-1

Perfect score: 260

Sequence: 1 HHPARTAHYGLPQKSHGRT.....VHFKNIVTPRPPSQGKG 46

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107396 residues

Total number of hits satisfying chosen parameters: 262820

Minimum DB seq length: 0

Maximum DB seq length: 27

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
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21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	139	53.5	25	17	AAW95342
2	139	53.5	25	18	AAW43948
3	135	51.9	24	15	AAW49336
4	135	51.9	24	16	AAW74158
5	135	51.9	24	19	AAW54719
6	135	51.9	24	22	AAU06294
7	135	51.9	24	22	AAG84534
8	135	51.9	24	22	AAG88287
9	135	51.9	24	22	AAG89383
10	135	51.9	24	22	AAJ00082
11	134	51.5	24	17	AAW95338

12	134	51.5	24	18	AAW37554	Human myelin basic MBP-2.2 (82-104).
13	129	49.6	23	17	AAW95339	Human myelin basic MBP-2.2 (82-104).
14	129	49.6	23	18	AAW37555	Human myelin basic MBP-2.2 (82-104).
15	128	49.2	23	16	AAW85137	Human myelin basic MBP-2.2 (82-104).
16	128	49.2	23	17	AAW95343	Human myelin basic MBP-2.2 (82-104).
17	128	49.2	23	17	AAW95337	Human myelin basic MBP-2.2 (82-104).
18	128	49.2	23	17	AAW44072	Human myelin basic MBP-2.2 (82-104).
19	128	49.2	23	18	AAW37553	Human myelin basic MBP-2.2 (82-104).
20	128	49.2	23	18	AAW43949	Human myelin basic MBP-2.2 (82-104).
21	128	49.2	23	19	AAW9785	Human myelin basic MBP-2.2 (82-104).
22	128	49.2	23	19	AAW4792	Human myelin basic MBP-2.2 (82-104).
23	128	49.2	23	21	AAW33602	Human myelin basic MBP-2.2 (82-104).
24	128	49.2	23	22	AAW93698	Human myelin basic MBP-2.2 (82-104).
25	128	49.2	24	17	AAW95386	Human myelin basic MBP-2.2 (82-104).
26	128	49.2	24	19	AAW50105	Human myelin basic MBP-2.2 (82-104).
27	118	45.4	21	17	AAW95341	Human myelin basic MBP-2.2 (82-104).
28	118	45.4	21	18	AAW43947	Human myelin basic MBP-2.2 (82-104).
29	118	45.4	21	18	AAW10302	Human myelin basic MBP-2.2 (82-104).
30	117	45.0	21	19	AAW54707	Human myelin basic MBP-2.2 (82-104).
31	117	45.0	21	22	AAU69216	Human myelin basic MBP-2.2 (82-104).
32	115	44.2	20	17	AAW95350	Human myelin basic MBP-2.2 (82-104).
33	115	44.2	20	18	AAW44062	Human myelin basic MBP-2.2 (82-104).
34	115	44.2	24	14	AAW46531	Human myelin basic MBP-2.2 (82-104).
35	114	43.8	21	17	AAW91923	Human myelin basic MBP-2.2 (82-104).
36	114	43.8	21	19	AAW72359	Human myelin basic MBP-2.2 (82-104).
37	112	43.1	20	17	AAW95392	Human myelin basic MBP-2.2 (82-104).
38	112	43.1	20	18	AAW34187	Human myelin basic MBP-2.2 (82-104).
39	112	43.1	20	18	AAW44064	Human myelin basic MBP-2.2 (82-104).
40	112	43.1	20	21	AAW26882	Human myelin basic MBP-2.2 (82-104).
41	110	42.3	20	17	AAW95391	Human myelin basic MBP-2.2 (82-104).
42	110	42.3	20	17	AAW95362	Human myelin basic MBP-2.2 (82-104).
43	110	42.3	20	18	AAW44063	Human myelin basic MBP-2.2 (82-104).
44	110	42.3	20	21	AAW33636	Human myelin basic MBP-2.2 (82-104).
45	110	42.3	20	22	AAW93732	Human myelin basic MBP-2.2 (82-104).

ALIGNMENTS

RESULT 1

ID AAR95342 standard; peptide; 25 AA.

AC AAR95342;

DT 16-DEC-1996 (first entry)

DE MBP-2.5 (80-104).

XX Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAP;
XX CD4+; T-cell; autoimmune disease; demyelination; central nervous system;
XX CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;
XX relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
XX diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;
XX psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
XX myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
OS Synthetic.

XX WO9612737-A2.

XX 02-MAY-1996.

XX 25-OCT-1995; 95WO-US13682.

XX 15-MAR-1995; 95US-0404228.

XX 25-OCT-1994; 94US-0328224.

XX 25-OCT-1995; 95ZA-0009033.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

XX Devaux B, Franzen H, Gefter M, Hsu D, Pallard X;

PI Rothbard J, Samson M, Shi J, Smilek D;

XX DR WPI; 1996-230552/23.
 XX PT Myelin basic derived peptide(s) and analogs - used in the treatment
 PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.
 XX PS Claim 1; Fig 2; 91pp; English.
 XX CC AAR95334-R95374 represent peptides derived from myelin basic protein
 CC (MBP). Immunisation with MBP can be used to induce experimental allergic
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+
 CC T-cell mediated autoimmune disease which results in demyelination of the
 CC central nervous system, resulting in paralysis and other neurological
 CC abnormalities. EAE is a commonly used animal model for human multiple
 CC sclerosis (MS). These sequences can be used in compositions for
 CC treating MS in a mammal. The composition acts to down regulate the
 CC autoimmune response, and may be administered in an amount sufficient to
 CC prevent the onset of symptoms of MS. The compositions may also be used
 CC to treat advanced stage MS, especially relapsing-remitting MS, chronic
 CC progressive MS or benign MS. These peptides may also be used in the
 CC treatment of other diseases involving myelin autoantigens, including
 CC psoriasis, Graves disease, myasthenia gravis, Good Pasture's syndrome,
 CC diabetes, thyroiditis, and rheumatoid arthritis. Peptides derived from
 CC other myelin autoantigens, such as myelin oligodendrocyte protein (MOG),
 CC proteolipid protein (PLP), and myelin associated glycoprotein (MAG) can
 CC be used as alternatives to these MBP peptides in these compositions.
 XX CC
 XX Sequence 25 AA;

Query Match 53.5%; Score 139; DB 17; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 TDQENPVVHFFKNIPTPTPPSQG 44
 DB 1 tqdenpvvhffknivtrtpppsqq 25

RESULT 2
 AAR43948
 ID AAR43948 standard; peptide; 25 AA.

XX AC AAR43948;

XX DT 22-APR-1998 (first entry)

XX DE Human myelin basic protein peptide MBP-2.5 (80-104).

XX KW Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
 KW autoimmune response; MBP; myelin basic protein; demyelinating.

XX OS Homo sapiens.

XX PN W09735879-AL.

XX PD 02-OCT-1997.

XX PF 01-MAY-1996; 96WO-US06072.

XX PR 28-MAR-1996; 96US-0623406.

XX PA (IMMU-) IMMULOGIC PHARM CORP.

XX PI Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;

XX DR WPI; 1997-489564/45.

XX PT Human myelin oligodendrocyte glyco-protein peptide - useful to treat
 PT multiple sclerosis in mammal by down-regulating auto-immune response

XX PS Claim 101; page 35; 108pp; English.

XX

CC The present sequence represents a novel peptide of human myelin
 CC basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte
 CC glycoprotein) and MBP can be used to treat multiple sclerosis in a
 CC mammal by down-regulating an autoimmune response in the mammal. They
 CC can also be used to diagnose and treat other demyelinating autoimmune
 CC diseases in humans, or to prepare antibodies for the detection or
 CC diagnosis of autoimmune diseases.

XX Sequence 25 AA;

Query Match 53.5%; Score 139; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 TDQENPVVHFFKNIPTPTPPSQG 44
 DB 1 tqdenpvvhffknivtrtpppsqq 25

RESULT 3

AAR49336

ID AAR49336 standard; Protein; 24 AA.

XX AC AAR49336;

XX DT 16-SEP-1994 (first entry)

XX DE Myelin basic protein position 75-98.

XX KW Naturally-occurring; immunomodulatory protein; human; therapy: class I;
 KW major histocompatibility complex; class II; allotype; type I diabetes;
 KW autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
 KW multiple sclerosis; transplant rejection; vaccine; MHC.

XX OS Homo sapiens.

XX PN W09404171-A.

XX PD 03-MAR-1994.

XX PF 11-AUG-1993; 93WO-US07545.

XX PR 11-AUG-1992; 92US-0925460.

XX PR 15-JUN-1993; 93US-0925460.

XX PA (HARD) HARVARD COLLEGE.

XX PI Chicx RM, Hedley ML, Stern LJ, Strominger JL, Urban RG;
 PI Vignali DA;

XX DR WPI; 1994-082825/10.

XX PT Novel immunomodulatory peptide(s) and nucleic acids - useful for
 PT treatment of auto-immune diseases, transplant rejection and for
 PT vaccination

XX PS Disclosure; page 38; 139pp; English.

XX CC The sequences given in AAR49291-505 and AAR46981-7038 represent peptide
 CC fragments of naturally-occurring immunomodulatory proteins. These
 CC fragments are between 10-30 residues in length and bind to a human
 CC major histocompatibility complex (MHC) class II allotype. These
 CC peptides may be used for therapy of autoimmune diseases, such as
 CC type I diabetes, rheumatoid arthritis and multiple sclerosis, and to
 CC reduce transplant rejection. They may also be used for vaccination
 CC providing an exclusively T-cell-mediated response, which can be
 CC class I or class-II based, or both, depending on the length and
 CC character of the immunogenic peptides.

XX Sequence 24 AA;

Query Match 51.9%; Score 135; DB 15; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.3e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GRTQDENPVVHFFKNIVTPRTPPP 41
 |||||
 DB 1 grtdenpvvhffknivtrtppp 24

RESULT 4

AAR74158
 ID AAR74158 standard; peptide; 24 AA.

XX AC AAR74158;

XX DT 03-AUG-1995 (first entry)

XX DE Antigenic peptide MBP 74-98.

XX KW Antigen; inhibitor; HA-specific T cell; MHC molecule; celiac disease;

XX KW food hypersensitivity; allergy; histocompatibility halo type;

XX KW Lyme Disease; hepatitis; post-streptococcal myocarditis;

XX KW glomerulonephritis.

XX OS Synthetic.

XX PN W09426774-A.

XX PD 24-NOV-1994.

XX PF 19-MAY-1994; 94WO-US05632.

XX PR 19-MAY-1993; 93US-0064298.

XX PA (CYTE-) CYTEL CORP.

XX PI Alexander J, Franco A, Grey HM, Sette AB;

XX DR WPI; 1995-006698/01.

XX PT Treatment of allergic diseases, partic. celiac disease - using a

XX PT peptide which binds a MHC molecule on an antigen presenting cell

XX PT to inhibit T cell activation

XX PS Example 1; Page 26; 52pp; English.

XX CC The sequences given in AAR74152-65 represent antigenic peptides which

XX CC were used in an example of the invention to demonstrate their

XX CC efficiency as inhibitors of an HA-specific T cell clone. These

XX CC peptides are examples of the peptides of the invention which are

XX CC capable of inhibiting celiac disease by binding to a MHC molecule on

XX CC an antigen presenting cell associated with celiac disease and this

XX CC inhibits the activation of a T cell associated with celiac disease.

XX CC These peptides can be used to treat other food hypersensitivities

XX CC and other allergic diseases associated with particular

XX CC histocompatibility halo types. They can be used to treat any

XX CC condition involving unwanted T-cell reactivity such as infectious

XX CC diseases that can cause immunopathology, eg. Lyme Disease, hepatitis,

XX CC post-streptococcal myocarditis or glomerulonephritis.

XX SQ Sequence 24 AA;

Query Match 51.9%; Score 135; DB 16; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.3e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GRTQDENPVVHFFKNIVTPRTPPP 41
 |||||
 DB 1 grtdenpvvhffknivtrtppp 24

RESULT 5

AAW54719

ID AAW54719 standard; peptide; 24 AA.

XX AC AAW54719;

XX DT 25-SEP-1998 (first entry)

XX DE Peptide from Myelin basic protein 75-98.

XX KW Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;

XX KW vaccine; treatment.

XX OS Synthetic.

XX PN W09813378-A1.

XX PD 02-APR-1998.

XX PF 25-SEP-1997; 97WO-NL00536.

XX PR 26-SEP-1996; 96EP-0202701.

XX PA (UYLE-) RIJKSUNIV LEIDEN.

XX PI Drijfhout JW, Koning F;

XX DR WPI; 1998-230631/20.

XX PT Increasing uptake and presentation of antigen(s) - by adding mannose

XX PT residue(s) to antigen for increasing T cell response, useful in,

XX PT e.g. vaccines against viral infection(s)

XX PS Disclosure; Page 33; 47pp; English.

XX CC The peptides AAW54559-W54809 are examples of peptides to which at least

XX CC 1 (preferably 2) mannose can be attached to increase their uptake as

XX CC antigens by antigen-presenting cells. Uptake of agonist mannosylated

XX CC peptides will increase the T cell response, whereas uptake of antagonist

XX CC peptides blocks the T cell response. Blocking binding of immunogenic

XX CC autoantigens can be used in treatment of type I diabetes, rheumatoid

XX CC arthritis, graft rejection etc., also to induce T-cell non-

XX CC responsiveness. Vaccines containing mannosylated antigen are used to

XX CC prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths

XX CC and parasites.

XX SQ Sequence 24 AA;

Query Match 51.9%; Score 135; DB 19; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.3e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GRTQDENPVVHFFKNIVTPRTPPP 41
 |||||
 DB 1 grtdenpvvhffknivtrtppp 24

RESULT 6

AAU06294
 ID AAU06294 standard; Peptide; 24 AA.

XX AC AAU06294;

XX DT 24-OCT-2001 (first entry)

XX DE Human Leukocyte Antigen (HLA) Class II standard supermotif peptide #6.

XX KW Prostate cancer-associated antigen; supermotif; human leukocyte antigen;

XX KW HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;

XX KW immunogenicity; immunosuppression; HTL.

XX OS Homo sapiens.

PN WO200145728-A2.
 PD 28-JUN-2001.
 XX
 XX 20-DEC-2000; 2000WO-US35516.
 XX 21-DEC-1999; 99US-0171312.
 XX 07-AUG-2000; 2000US-0633364.
 XX (EPIM-) EPIMMUNE INC.
 XX
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cellis E;
 XX Keogh E;
 XX WPI; 2001-398311/42.
 XX
 XX Tumour antigen-associated group-based vaccines useful for vaccinating
 XX against prostate cancer -
 XX
 XX Example 1; Page 86; 252pp; English.
 XX
 XX The sequences represent prostate cancer-associated antigens and derived
 XX motif or supermotif epitopes. The peptide epitopes are included in
 XX prostate cancer vaccine compositions due to their ability to bind to
 XX human leukocyte antigen (HLA) molecules, which recognise the motifs.
 XX peptides with a high binding affinity are further tested for their
 XX ability to induce a cytotoxic T lymphocyte (CTL) or a helper T lymphocyte
 XX (HTL) response. Supermotif-bearing peptides may also be tested for their
 XX binding affinity to multiple alleles within the HLA superfamily. The
 XX vaccine compositions can be modified, for example, to enhance
 XX immunogenicity, to avoid the inclusion of immunosuppressive groups, or to
 XX alter the immune response to suit the target disease. These group-based
 XX vaccines allow the focus of an immune response to multiple selected
 XX antigens from the same pathogen. Variability among the immune responses
 XX of patients can therefore be alleviated by the inclusion of groups from
 XX multiple antigens in a vaccine.
 XX
 XX Sequence 24 AA;

Query Match 51.9%; Score 135; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.3e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GRTODENPVVHFKNIVTRTPPP 41
 DB 1 grtdenpvvhnfvtrtppp 24

RESULT 7
 AAG84534
 ID AAG84534 standard; Peptide; 24 AA.
 XX
 XX AAG84534;
 XX
 XX 10-SEP-2001 (first entry)

XX Human leukocyte antigen (HLA) class II binding peptide DRB1*1501.
 XX
 XX Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte;
 XX CTL; MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine;
 XX cancer; cytostatic; immunostimulant.
 XX
 XX Homo sapiens.
 XX Synthetic.
 XX
 XX WO200142267-A1.
 XX
 XX 14-JUN-2001.
 XX
 XX 11-DEC-2000; 2000WO-US33545.
 XX
 XX 10-DEC-1999; 99US-0458298.

XX (EPIM-) EPIMMUNE INC.
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cellis E;
 XX Keogh E;
 XX WPI; 2001-375002/39.
 XX
 XX An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
 XX the treatment and prevention of cancer -
 XX
 XX Disclosure; Page 84; 171pp; English.

XX The present invention describes MAGE2/3 epitopes (I). Also described
 XX are: (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo
 XX and binds to a complex of (I); (2) a peptide (II) comprising (I) and a
 XX second epitope and has less than 50 contiguous amino acids; (3) a vaccine
 XX composition comprising (II), a unit dose of a peptide with at least 50
 XX contiguous amino acids with 100% identity to the native peptide sequence
 XX of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
 XX encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
 XX cytostatic activity, and can be used in vaccines and as an
 XX immunostimulant. A vaccine of (3) is useful for the treatment and
 XX prevention of cancer. (I) is useful for monitoring or evaluating an
 XX immune response by incubating a T-lymphocyte sample from a patient with
 XX (I) that binds to an human leukocyte antigen (HLA) allele present in the
 XX patient and detecting the presence of the T-lymphocyte that binds to the
 XX peptide. The vaccine allows the opportunity to combine epitopes derived
 XX from multiple tumour-associated molecules reducing the likelihood of
 XX tumour escape due to antigen loss. MAGE2/3 to AAG84515 and AAG89725
 XX represent amino acid sequences used in the exemplification of the
 XX present invention.

XX Sequence 24 AA;

Query Match 51.9%; Score 135; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.3e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GRTODENPVVHFKNIVTRTPPP 41
 DB 1 grtdenpvvhnfvtrtppp 24

RESULT 8
 AAG88287
 ID AAG88287 standard; Peptide; 24 AA.
 XX
 XX AAG88287;
 XX
 XX 11-SEP-2001 (first entry)

XX Human leukocyte antigen (HLA) class II binding peptide DRB1*1501.
 XX
 XX Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
 XX immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
 XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
 XX
 XX Homo sapiens.
 XX Synthetic.
 XX
 XX WO200141787-A1.
 XX
 XX 14-JUN-2001.
 XX
 XX 11-DEC-2000; 2000WO-US33591.
 XX
 XX 10-DEC-1999; 99US-0458299.

XX (EPIM-) EPIMMUNE INC.
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cellis E;

PI Keogh E;
 XX WPI; 2001-374995/39.
 XX An isolated prepared HER2/neu epitope useful in a vaccine for inducing
 XX cellular immune responses for the prevention and treatment of cancer.
 XX
 XX Disclosure; Page 84; 199pp; English.
 XX
 XX The present invention describes isolated prepared HER2/neu epitopes (I).
 XX Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
 XX culture in vitro and binds to a complex of an epitope (I), bound to a
 XX human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
 XX and a second epitope and the peptide is less than 50 contiguous amino
 XX acids that have 100% identity with a native peptide sequence of HER2/neu;
 XX (3) a vaccine composition (III) comprising (II) and a pharmaceutical
 XX excipient; (4) an isolated nucleic acid encoding a peptide comprising
 XX (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic
 XX and immunostimulant activities, and can be used in vaccines. (I), (II)
 XX and (III) are useful for inducing cellular immune responses for the
 XX prevention and treatment of cancer. (I) and (II) are useful for
 XX monitoring or evaluating an immune response to a tumour-associated
 XX antigen when incubated with a T lymphocyte sample from a patient and
 XX detecting the presence of bound T lymphocyte to (I) or (II). Epitope
 XX based vaccines mean that immunosuppressive epitopes that may be present
 XX in whole antigens may be avoided. Selected epitopes may be combined to
 XX enhance immunogenicity. The possible pathological side effects caused by
 XX infectious agents or whole protein antigen is eliminated. The vaccine
 XX provides the ability to direct and focus an immune response to multiple
 XX selected antigens from the same pathogen. Epitope-based anti-tumour
 XX vaccines provides the opportunity to combine epitopes derived from
 XX multiple tumour-associated molecules addressing the problem of tumour-
 XX tumour variability and reducing the likelihood of tumour escape due to
 XX antigen loss. AAG8266 to AAG89121 represent amino acid sequences used in
 XX the exemplification of the present invention.
 XX
 XX Sequence 24 AA;

Query Match 51.9%; Score 135; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.3e-11;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GRTQDENPVVHFFKNIVTRTPPP 41
 |||||
 Db 1 grtqdenpvvhffknivtrtppp 24

RESULT 9

AAG89383
 ID AAG89383 standard; Peptide; 24 AA.

XX AAG89383;

XX 11-SEP-2001 (first entry)

XX Human leukocyte antigen (HLA) class II binding peptide DRB1*1501.

XX Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;

XX cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;
 XX vaccine; epitope; cytostatic.

XX Homo sapiens.

XX Synthetic.

XX WO200141788-A1.

XX 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US33629.

XX 10-DEC-1999; 99US-0458297.

PA (EPIM-) EPIMMUNE INC.
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;
 XX Keogh E;
 XX WPI; 2001-381493/40.
 XX
 XX Epitope-based vaccines comprising p53 epitope having a specified
 XX sequences, useful for treating and preventing cancer, the epitopic
 XX peptides is useful as diagnostic agents and for evaluating immune
 XX response -
 XX
 XX Disclosure; Page 83; 138pp; English.

XX The present invention describes isolated prepared p53 epitopes (I). Also
 XX described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured
 XX in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I)
 XX and a second epitope and has less than 50 contiguous amino acids; (3) a
 XX vaccine composition comprising (II), a unit dose of a peptide with less
 XX than 50 contiguous amino acids with 100% identity to the native peptide
 XX sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic
 XX acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)
 XX has cytostatic activity and can be used in vaccines. The vaccine
 XX composition is useful for treating or preventing cancer. (I) and (II)
 XX are useful as diagnostic agents and for evaluating immune responses.
 XX Unlike conventional epitopes, immunosuppressive epitopes that may be
 XX present in whole antigens can be avoided with the use of the vaccine
 XX composition of (I). The ability to combine selected epitopes and
 XX further, to modify the composition of the epitopes enhances the
 XX immunogenicity. The possible pathological side effects caused by
 XX infectious agents or whole protein antigens, which might have their own
 XX intrinsic biological activity, are eliminated. AAG89363 to AAG89747
 XX represent amino acid sequences used in the exemplification of the
 XX present invention.

XX Sequence 24 AA;

Query Match 51.9%; Score 135; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.3e-11;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GRTQDENPVVHFFKNIVTRTPPP 41
 |||||
 Db 1 grtqdenpvvhffknivtrtppp 24

RESULT 10

AAJ00082

ID AAJ00082 standard; Peptide; 24 AA.

XX AAJ00082;

XX 02-JUL-2001 (first entry)

XX Hepatitis C virus epitope #73.

XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 XX antiviral.

XX Hepatitis C virus.

XX WO200121189-A1.

XX 29-MAR-2001.

XX 19-JUL-2000; 2000WO-US19774.

XX 19-JUL-1999; 99US-0357737.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Cells E, Kubo RT, Grey HM;
 XX WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus -
 XX
 PS Example 1; Page 101; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ0010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 24 AA;

Query Match 51.9%; Score 135; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.3e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GRTQDENPVVHFFKNIVTPTPTPP 41
 |||||
 DB 1 grtqdenpvvhffknivtptpp 24

RESULT 11
 AAR95338
 ID AAR95338 standard; peptide; 24 AA.
 XX
 AC AAR95338;
 XX
 DT 16-DEC-1996 (first entry)
 XX
 DE MBP-2.1 (82-105).
 XX
 KW Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
 KW CD4+; T-cell; autoimmune disease; demyelination; central nervous system;
 KW CNS; animal model; human; multiple sclerosis; MS; benign MS; MOG;
 KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
 KW diabetes; Graves disease; myasthenia gravis; Good pasture's syndrome;
 KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
 KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
 XX
 OS Synthetic.
 XX
 XX WO9612737-A2.
 PN
 PD 02-MAY-1996.
 XX
 PF 25-OCT-1995; 95WO-US13682.
 XX
 PR 15-MAR-1995; 95US-0404228.
 PR 25-OCT-1994; 94US-0328224.
 PR 25-OCT-1995; 95ZA-0009033.
 XX
 PA (IMMU-) IMMULOGIC PHARM CORP.
 XX
 PI Devaux B, Franzen H, Geffer M, Hsu D, Paliard X;
 PI Rothbard J, Samson M, Shi J, Smilek D;
 XX
 DR WPI; 1996-230552/23.
 XX
 PT Myelin basic derived peptide(s) and analogs - used in the treatment
 PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.
 XX
 PS Claim 1; Fig 2; 91pp; English.
 XX
 CC AAR95334-R95374 represent peptides derived from myelin basic protein
 CC (MBP). Immunisation with MBP can be used to induce experimental allergic
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+
 CC T-cell mediated autoimmune disease which results in demyelination of the
 CC central nervous system, resulting in paralysis and other neurological

CC abnormalities. EAE is a commonly used animal model for human multiple
 CC sclerosis (MS). These sequences can be used in compositions for
 CC treating MS in a mammal. The composition acts to down regulate the
 CC autoimmune response, and may be administered in an amount sufficient to
 CC prevent the onset of symptoms of MS. The compositions may also be used
 CC to treat advanced stage MS, especially relapsing-remitting MS, chronic
 CC progressive MS or benign MS. These peptides may also be used in the
 CC treatment of other diseases involving myelin autoantigens, including
 CC diabetes, Graves disease, myasthenia gravis, Good pasture's syndrome,
 CC psoriasis, thyroiditis, and rheumatoid arthritis. Peptides derived from
 CC other myelin autoantigens, such as myelin oligodendrocyte protein (MOG),
 CC proteolipid protein (PLP), and myelin associated glycoprotein (MAG) can
 CC be used as alternatives to these MBP peptides in these compositions.
 XX

SQ Sequence 24 AA;

Query Match 51.5%; Score 134; DB 17; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 DENPVVHFFKNIVTPTPTPPSGK 45
 |||||
 DB 1 denpvvhffknivtptppsgk 24

RESULT 12
 AAR95354
 ID AAR95354 standard; peptide; 24 AA.
 XX
 AC AAR95354;
 XX
 DT 22-APR-1998 (first entry)
 XX
 DE Human myelin basic protein peptide MBP-2.1 (82-105).
 XX
 KW Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
 KW autoimmune response; MBP; myelin basic protein; demyelinating.
 XX
 OS Homo sapiens.
 XX
 PN WO9735879-A1.
 XX
 PD 02-OCT-1997.
 XX
 PF 01-MAY-1996; 96WO-US06072.
 XX
 PR 28-MAR-1996; 96US-0623406.
 XX
 PA (IMMU-) IMMULOGIC PHARM CORP.
 XX
 PI Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;
 XX
 DR WPI; 1997-489564/45.
 XX
 PT Human myelin oligodendrocyte glyco-protein peptide - useful to treat
 PT multiple sclerosis in mammal by down-regulating auto-immune response
 XX
 PS Claim 101; Page 35; 108pp; English.
 XX
 CC The present sequence represents a novel peptide of human myelin
 CC basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte
 CC glycoprotein) and MBP can be used to treat multiple sclerosis in a
 CC mammal by down-regulating an autoimmune response in the mammal. They
 CC can also be used to diagnose and treat other demyelinating autoimmune
 CC diseases in humans, or to prepare antibodies for the detection or
 CC diagnosis of autoimmune diseases.
 XX
 SQ Sequence 24 AA;

Query Match 51.5%; Score 134; DB 18; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.1e-10;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFKNIVTPTPTPPSQK 45
 |||||
 DB 1 denpvvhfkniivtptppsqgk 24

RESULT 13
 AAR95339
 ID AAR95339 standard; peptide: 23 AA.
 XX
 AC AAR95339;
 XX
 DT 16-DEC-1996 (first entry)
 XX
 DE MBP-2.2 (82-104).
 XX
 KW Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
 KW CD4+; T-cell; autoimmune disease; demyelination; central nervous system;
 KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;
 KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
 KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;
 KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
 KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
 XX
 OS Synthetic.
 XX
 PN WO9612737-A2.
 PD 02-MAY-1996.
 XX
 PF 25-OCT-1995; 95WO-US13682.
 XX
 PR 15-MAR-1995; 95US-0404228.
 PR 25-OCT-1994; 94US-0328224.
 PR 25-OCT-1995; 95ZA-0009033.
 XX
 PA (IMMU-) IMMULOGIC PHARM CORP.
 XX
 PI Devaux B, Franzen H, Geftter M, Hsu D, Paliard X;
 PI Rothbard J, Samson M, Shi J, Smilek D;
 XX
 DR WPI; 1996-230552/23.
 XX
 PT Myelin basic derived peptide(s) and analogs - used in the treatment
 PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.
 XX
 PS Claim 1; Fig 2; 91pp; English.
 XX
 CC AAR95334-R95374 represent peptides derived from myelin basic protein
 CC (MBP). Immunisation with MBP can be used to induce experimental allergic
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+
 CC T-cell mediated autoimmune disease which results in demyelination of the
 CC central nervous system, resulting in paralysis and other neurological
 CC abnormalities. EAE is a commonly used animal model for human multiple
 CC sclerosis (MS). These sequences can be used in compositions for
 CC treating MS in a mammal. The composition acts to down regulate the
 CC autoimmune response, and may be administered in an amount sufficient to
 CC prevent the onset of symptoms of MS. The compositions may also be used
 CC to treat advanced stage MS, especially relapsing-remitting MS, chronic
 CC progressive MS or benign MS. These peptides may also be used in the
 CC treatment of other diseases involving myelin autoantigens, including
 CC diabetes, Graves disease, myasthenia gravis, Good Pasture's syndrome,
 CC psoriasis, thyroiditis, and rheumatoid arthritis. Peptides derived from
 CC other myelin autoantigens, such as myelin oligodendrocyte protein (MOG),
 CC proteolipid protein (PLP), and myelin associated glycoprotein (MAG) can
 CC be used as alternatives to these MBP peptides in these compositions.
 XX
 SQ Sequence 23 AA;

Query Match 49.6%; Score 129; DB 17; Length 23;
 Best Local Similarity 100.0%; Pred. No. 4.8e-10;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFKNIVTPTPTPPSQK 45
 |||||
 DB 1 denpvvhfkniivtptppsqgk 24

RESULT 14
 AAW37555
 ID AAW37555 standard; peptide: 23 AA.
 XX
 AC AAW37555;
 XX
 DT 22-APR-1998 (first entry)
 XX
 DE Human myelin basic protein peptide MBP-2.2 (82-104).
 XX
 KW Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
 KW autoimmune response; MBP; myelin basic protein; demyelinating.
 XX
 OS Homo sapiens.
 XX
 PN WO9735879-A1.
 PD 02-OCT-1997.
 XX
 PF 01-MAY-1996; 96WO-US06072.
 XX
 PR 28-MAR-1996; 96US-0623406.
 XX
 PA (IMMU-) IMMULOGIC PHARM CORP.
 XX
 PI Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;
 XX
 DR WPI; 1997-489564/45.
 XX
 PT Human myelin oligodendrocyte glyco-protein peptide - useful to treat
 PT multiple sclerosis in mammal by down-regulating auto-immune response
 XX
 PS Claim 101; Page 35; 108pp; English.
 XX
 CC The present sequence represents a novel peptide of human myelin
 CC basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte
 CC glycoprotein) and MBP can be used to treat multiple sclerosis in a
 CC mammal by down-regulating an autoimmune response in the mammal. They
 CC can also be used to diagnose and treat other demyelinating autoimmune
 CC diseases in humans, or to prepare antibodies for the detection or
 CC diagnosis of autoimmune diseases.
 XX
 SQ Sequence 23 AA;

Query Match 49.6%; Score 129; DB 18; Length 23;
 Best Local Similarity 100.0%; Pred. No. 4.8e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFKNIVTPTPTPPSQG 44
 |||||
 DB 1 denpvvhfkniivtptppsqg 23

RESULT 15
 AAR85137
 ID AAR85137 standard; peptide: 23 AA.
 XX
 AC AAR85137;
 XX
 DT 18-JUN-1996 (first entry)
 XX
 DE Human MBP residues 84-106 (MBP 84-106).
 XX
 KW Myelin basic protein; MBP; human; antigenic peptide; interferon-beta;
 KW IFN-beta; multiple sclerosis; experimental allergic encephalomyelitis;

XX 15-MAR-1995; 95US-0404228.
 PR 25-OCT-1994; 94US-0328224.
 PR 25-OCT-1995; 95ZA-0009033.
 XX
 PA (IMMU-) IMMULOGIC PHARM CORP.
 XX
 XX Devaux B, Franzen H, Geftter M, Hsu D, Paliard X;
 PI Rothbard J, Samson M, Shi J, Smilek D;
 PI WPI; 1996-230552/23.
 XX
 XX Myelin basic derived peptide(s) and analogs - used in the treatment
 PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.
 XX
 PS Claim 1; Fig 2; 91pp; English.
 XX
 CC AAR95334-R95374 represent peptides derived from myelin basic protein
 CC (MBP). Immunisation with MBP can be used to induce experimental allergic
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+
 CC T-cell mediated autoimmune disease which results in demyelination of the
 CC central nervous system, resulting in paralysis and other neurological
 CC abnormalities. EAE is a commonly used animal model for human multiple
 CC sclerosis (MS). These sequences can be used in compositions for
 CC treating MS in a mammal. The composition acts to down regulate the
 CC autoimmune response, and may be administered in an amount sufficient to
 CC prevent the onset of symptoms of MS. The compositions may also be used
 CC to treat advanced stage MS, especially relapsing-remitting MS, chronic
 CC progressive MS or benign MS. These peptides may also be used in the
 CC treatment of other diseases involving myelin autoantigens, including
 CC diabetes, Graves disease, myasthenia gravis, Good Pasture's syndrome,
 CC psoriasis, thyroiditis, and rheumatoid arthritis. Peptides derived from
 CC other myelin autoantigens, such as myelin oligodendrocyte protein (MOG),
 CC proteolipid protein (PLP), and myelin associated glycoprotein (MAG) can
 CC be used as alternatives to these MBP peptides in these compositions.
 XX
 SQ Sequence 23 AA;
 XX
 Query Match 49.2%; Score 128; DB 17; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.5e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 23 ENPVVHFFKNIVTPRTPPSQGK 45
 Db 1 ENPVVHFFKNIVTPRTPPSGK 23
 XX
 RESULT 18
 AAW44072
 ID AAW44072 standard; peptide; 23 AA.
 XX
 AC AAW44072;
 XX
 DT 22-APR-1998 (first entry)
 XX
 DE Human myelin basic protein peptide MBP-R (83-105).
 XX
 KW Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
 KW autoimmune response; MBP; myelin basic protein; demyelinating.
 XX
 OS Homo sapiens.
 XX
 PN WO9735879-A1.
 XX
 PD 02-OCT-1997.
 XX
 PF 01-MAY-1996; 96WO-US06072.
 XX
 PR 28-MAR-1996; 96US-0623406.
 XX
 PA (IMMU-) IMMULOGIC PHARM CORP.
 XX
 PI Devaux B, Franzen H, Geftter M, Hsu D, Paliard X, Smilek D, Wallner B;
 PI WPI; 1997-489564/45.
 XX
 DR Human myelin oligodendrocyte glyco-protein peptide - useful to treat
 DR multiple sclerosis in mammal by down-regulating auto-immune response
 XX
 Claim 101; Page 35; 108pp; English.
 XX
 CC The present sequence represents a novel peptide of human myelin
 CC basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte
 CC glycoprotein) and MBP can be used to treat multiple sclerosis in a
 CC mammal by down-regulating an autoimmune response in the mammal. They
 CC can also be used to diagnose and treat other demyelinating autoimmune
 CC diseases in humans, or to prepare antibodies for the detection or
 CC diagnosis of autoimmune diseases.
 XX
 SQ Sequence 23 AA;

PI Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;
 XX WPI; 1997-489564/45.
 DR
 XX Human myelin oligodendrocyte glyco-protein peptide - useful to treat
 PT multiple sclerosis in mammal by down-regulating auto-immune response
 XX
 PS Disclosure; Page 35; 108pp; English.
 XX
 CC The present sequence represents a novel peptide of human myelin
 CC basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte
 CC glycoprotein) and MBP can be used to treat multiple sclerosis in a
 CC mammal by down-regulating an autoimmune response in the mammal. They
 CC can also be used to diagnose and treat other demyelinating autoimmune
 CC diseases in humans, or to prepare antibodies for the detection or
 CC diagnosis of autoimmune diseases.
 XX
 SQ Sequence 23 AA;
 XX
 Query Match 49.2%; Score 128; DB 18; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.5e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 23 ENPVVHFFKNIVTPRTPPSQGK 45
 Db 1 ENPVVHFFKNIVTPRTPPSGK 23
 XX
 RESULT 19
 AAW37553
 ID AAW37553 standard; peptide; 23 AA.
 XX
 AC AAW37553;
 XX
 DT 22-APR-1998 (first entry)
 XX
 DE Human myelin basic protein peptide MBP-2 (83-105).
 XX
 KW Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
 KW autoimmune response; MBP; myelin basic protein; demyelinating.
 XX
 OS Homo sapiens.
 XX
 PN WO9735879-A1.
 XX
 PD 02-OCT-1997.
 XX
 PF 01-MAY-1996; 96WO-US06072.
 XX
 PR 28-MAR-1996; 96US-0623406.
 XX
 PA (IMMU-) IMMULOGIC PHARM CORP.
 XX
 PI Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;
 PI WPI; 1997-489564/45.
 XX
 DR Human myelin oligodendrocyte glyco-protein peptide - useful to treat
 DR multiple sclerosis in mammal by down-regulating auto-immune response
 XX
 PS Claim 101; Page 35; 108pp; English.
 XX
 CC The present sequence represents a novel peptide of human myelin
 CC basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte
 CC glycoprotein) and MBP can be used to treat multiple sclerosis in a
 CC mammal by down-regulating an autoimmune response in the mammal. They
 CC can also be used to diagnose and treat other demyelinating autoimmune
 CC diseases in humans, or to prepare antibodies for the detection or
 CC diagnosis of autoimmune diseases.
 XX
 SQ Sequence 23 AA;

Query Match 49.2%; Score 128; DB 18; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.5e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 ENPVVHFFKNIVTRTPPPSGK 45
 Db 1 enpvvhffknivtrtpppsgk 23

RESULT 20

AAW43949

ID AAW43949 standard; peptide; 23 AA.

XX AAW43949;

XX 22-APR-1998 (first entry)

XX Human myelin basic protein peptide MBP-2.6 (80-102).

XX Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
 XX autoimmune response; MBP; myelin basic protein; demyelinating.

XX Homo sapiens.

XX WO9735879-A1.

XX 02-OCT-1997.

XX 01-MAY-1996; 96WO-US06072.

XX 28-MAR-1996; 96US-0623406.

XX (IMMU-) IMMULOGIC PHARM CORP.

XX Devaux B., Garman RD., Rothbard J., Smilek D., Wallner B;

XX WPI; 1997-489564/45.

XX Human myelin oligodendrocyte glyco-protein peptide - useful to treat
 XX multiple sclerosis in mammal by down-regulating auto-immune response

XX Claim 101; Page 35; 108pp; English.

XX The present sequence represents a novel peptide of human myelin
 XX basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte
 XX glycoprotein) and MBP can be used to treat multiple sclerosis in a
 XX mammal by down-regulating an autoimmune response in the mammal. They
 XX can also be used to diagnose and treat other demyelinating autoimmune
 XX diseases in humans, or to prepare antibodies for the detection or
 XX diagnosis of autoimmune diseases.

XX Sequence 23 AA;

Query Match 49.2%; Score 128; DB 18; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.5e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 TODENPVVHFFKNIVTRTPPPS 42
 Db 1 tqdenpvvhffknivtrtppps 23

RESULT 21

AAW69765

ID AAW69765 standard; peptide; 23 AA.

XX AAW69765;

XX 17-NOV-1998 (first entry)

XX Myelin basic protein fragment 80-102.

XX

KW Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
 KW class II associated peptide; pathogen; gene therapy; genetic disease;
 KW infection; downregulation; immune response.

XX Homo sapiens.

XX Synthetic.

XX WO9831398-A1.

XX 23-JUL-1998.

XX 22-JAN-1998; 98WO-US01499.

XX 06-JAN-1998; 98US-0003253.

XX 22-JAN-1997; 97US-0787547.

XX (PANG-) PANGAEA PHARM INC.

XX Curley JM, Hedley ML, Langer RS, Lunsford LB;

XX WPI; 1998-427556/36.

XX New preparations of microparticles - comprising a synthetic polymer
 XX matrix and nucleic acid comprising an expression vector for use in
 XX gene therapy

XX Example 10; Page 54; 101pp; English.

XX

XX A microparticle preparation (MP) has been developed, consisting of
 XX microparticles having a diameter of less than 100 nm. The MP
 XX comprises: (a) a polymeric matrix (PM) consisting of one or more
 XX synthetic polymers having a solubility in water of less than 1 mg/L; and
 XX (b) an expression vector selected from RNA molecules (at least 50% of
 XX which are closed circles) or circular plasmid DNA (at least 50% of which
 XX are supercoiled). Also described is a MP of at most 20 microns in
 XX diameter, comprising: (a) a PM; and (b) a NAM comprising an expression
 XX control sequence operatively linked to a coding sequence, where the
 XX coding sequence encodes an expression product selected from: (1) a
 XX polypeptide at least 7 amino acids in length, having a sequence identical
 XX to the sequence of: (i) a fragment of a naturally-occurring mammalian
 XX protein; or (ii) a fragment of a naturally-occurring protein from an
 XX infectious agent which infects a mammal; (2) a peptide having a length
 XX and sequence which permits it to bind to an MHC class I or II molecule;
 XX and (3) the polypeptide or the peptide linked to a trafficking sequence.
 XX AAW69763 to AAW69765, and AAW78793 to AAW78897 are peptide fragments for
 XX use in the present invention. The MPs are highly effective vehicles for
 XX the delivery of polynucleotides into phagocytic cells. They can be used
 XX for gene therapy, e.g. for treating genetic diseases, infections or
 XX tumours or for downregulating an immune response.

XX Sequence 23 AA;

Query Match 49.2%; Score 128; DB 19; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.5e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GRTQDENPVVHFFKNIVTRTPPP 40
 Db 1 grtqdenpvvhffknivtrtppp 23

RESULT 22

AAW64792

ID AAW64792 standard; peptide; 23 AA.

XX AAW64792;

XX 29-SEP-1998 (first entry)

XX MBP 80-102.

XX

KW Myelin basic protein; MBP; gene therapy; multiple sclerosis;
 KW microparticle; autoantigen; autoimmune disease; MHC.
 XX Homo sapiens.
 OS
 PN US5783567-A.
 XX
 PD 21-JUL-1998.
 XX
 PF 22-JAN-1997; 97US-0787547.
 XX
 PR 22-JAN-1997; 97US-0787547.
 XX
 PA (PANG-) PANGAEA PHARM INC.
 XX
 PI Curley JM, Hedley ML, Langer RS;
 XX
 DR WPI; 1998-427077/36.
 XX
 PT Microparticle encapsulated nucleic acids - for recombinant
 PT expression of proteins e.g. in gene therapy
 XX
 PS Disclosure; Column 4; 42pp; English.
 XX
 CC The patent describes a new preparation of microparticles each
 CC comprising a polymeric matrix and a nucleic acid. The polymeric
 CC matrix consists of one or more synthetic polymers having a solubility
 CC in water of less than 1 mg/l (e.g. poly-lactic-co-glycolic acid);
 CC and at least 90% of the microparticles have a diameter of less than
 CC 100 microns. The microparticles are useful for the delivery of nucleic
 CC acids to phagocytic cells. In one embodiment the microparticles are
 CC less than 20 microns in diameter and the nucleic acid (preferably in
 CC closed circular form) includes an expression control sequence
 CC operatively linked to a coding sequence, where the expression product
 CC of the coding sequence is a polypeptide having a length and a sequence
 CC which permits it to bind to an MHC class I or II molecule. The
 CC expression product is thus an effective stimulator of an immune
 CC response in mammals. The present sequence, an antigenic portion of
 CC myelin basic protein (MBP), is an example of an MHC class II peptide
 CC which can be expressed by the nucleic acid. It is associated with
 CC multiple sclerosis.
 XX
 SQ Sequence 23 AA;

Query Match 49.2%; Score 128; DB 19; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.5e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GRTQDENPVVHFFKNIVTPRTPP 40
 |||||
 DB 1 grtqdenpvvhffknivtrtp 23

RESULT 23
 AAB33602
 ID AAB33602 standard; Peptide; 23 AA.
 XX
 AC AAB33602;
 XX
 DT 26-JAN-2001 (first entry)
 XX
 DE MHC class II associated immunogenic peptide SEQ ID 1.
 XX
 KW Microparticle; nucleic acid delivery; immunogenic peptide; MHC II;
 KW major histocompatibility complex; vaginal tissue; mucosal tissue..
 XX
 OS Unidentified.
 XX
 PN WO200053161-A2.
 XX
 PD 14-SEP-2000.
 XX

PF 10-MAR-2000; 2000WO-US06578.
 XX
 PR 11-MAR-1999; 99US-0266463.
 PR 27-MAY-1999; 99US-0321346.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Lunsford LB, Putnam D, Hedley ML;
 XX
 DR WPI; 2000-638130/61.
 XX
 PT Microparticles useful for administering a nucleic acid into the mucosal
 PT tissue preferably vaginal tissue of an animal, comprises a polymeric
 PT matrix, a lipid and a nucleic acid molecule -
 XX
 PS Claim 25; Page 10; 96pp; English.
 XX
 CC The present invention relates to microparticles which are less than 20
 CC microns in diameter, which comprise a polymeric matrix, a lipid and a
 CC nucleic acid molecule. The microparticle is specifically not
 CC encapsulated in a liposome and does not comprise a cell. The nucleotide
 CC sequence encodes an expression product that binds to major
 CC histocompatibility complex (MHC) type I or II molecules. Peptides
 CC AAB33602-B33647 represent MHC class II associated immunogenic peptides,
 CC and AAB33648-B33710 represent MHC class I associated immunogenic
 CC peptides. The peptides are examples of the expression products of the
 CC nucleotide sequences which can be included in the microparticles of the
 CC invention. Sequences AAB33711-B33716 represent alternative expression
 CC products and nuclear localisation signals also used in the invention. The
 CC microparticles are useful for administering a nucleic acid into the
 CC mucosal tissue preferably vaginal tissue of an animal.
 XX
 SQ Sequence 23 AA;

Query Match 49.2%; Score 128; DB 21; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.5e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 GRTQDENPVVHFFKNIVTPRTPP 40
 |||||
 DB 1 grtqdenpvvhffknivtrtp 23

RESULT 24
 AAG93698
 ID AAG93698 standard; Peptide; 23 AA.
 XX
 AC AAG93698;
 XX
 DT 17-SEP-2001 (first entry)
 XX
 DE Human myelin basic protein peptide 1.
 XX
 KW Continuous flow production; microparticle; gene therapy;
 KW antisense therapy; vaccination; treatment; autoimmune disease;
 KW immune response modulation.
 XX
 OS Homo sapiens.
 XX
 PN WO200136583-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-US31770.
 XX
 PR 19-NOV-1999; 99US-0443654.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Hedley ML, Hsu Y, Tyo M;
 XX
 DR WPI; 2001-425203/45.
 XX

XX Continuous production of microparticles containing nucleic acid for
 PT e.g. gene therapy, comprises mixing a solution of polymeric material
 PT and nucleic acid with a surfactant solution, removing solvent and
 PT drying -
 XX
 PS Disclosure; Page 9; 47pp; English.
 XX
 CC The present sequence is that of a peptide of the invention.
 CC The invention relates to a method for scalable, continuous flow
 CC production of a nucleic acid containing microparticle that maintains the
 CC structural integrity of the associated nucleic acid and results in a
 CC microparticle having purity suitable for introduction into an animal
 CC host. Microparticles prepared according to the method can be used for
 CC delivery of a nucleic acid for gene therapy, antisense therapy,
 CC vaccination, treatment of autoimmune disease and either specific or
 CC non-specific modulation of an immune response. The microparticles may
 CC also be used to deliver nucleic acid encoding a protein or peptide useful
 CC in any kind of therapy. The method is economical, aseptic and scalable.
 CC The method also enables control over the size of microparticles. The
 CC microparticles produced are free of impurities such as organic solvents
 CC and are readily dispersed in a wide range of dispersing agents.
 XX
 SQ Sequence 23 AA;

Query Match 49.2%; Score 128; DB 22; Length 23;
 Best Local Similarity 100.0%; Pred. No. 6.5e-10;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GRTQDENPVVHFKNIVTPRTPP 40
 DB 1 grtdenpvvhfkniivtrtp 23

RESULT 25
 AAR95386
 ID AAR95386 standard; peptide; 24 AA.
 AC AAR95386;
 XX
 DT 16-DEC-1996 (first entry)
 XX
 DE MBP-2.1 (82-105) [K91A].

XX Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
 KW CD4+; T-cell; autoimmune disease; demyelination; central nervous system;
 KW CNS; animal model; human; multiple sclerosis; MS; mammal; Denign MS; MOG;
 KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
 KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;
 KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
 KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
 XX
 OS Synthetic.

XX
 XX Key Location/Qualifiers
 FH Misc-difference 10
 FT /note= "K91A"

FT W09612737-A2.

XX 02-MAY-1996.

XX 25-OCT-1995; 95WO-USL3682.

XX 15-MAR-1995; 95US-0404228.

XX 25-OCT-1994; 94US-0328224.

XX 25-OCT-1995; 95ZA-0009033.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

XX Devaux B, Franzen H, Geffer M, Hsu D, Pallard X;
 PI Rothbard J, Samson M, Shi J, Smilek D;

XX WPI; 1996-230552/23.
 XX Myelin basic derived peptide(s) and analogs - used in the treatment
 PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.
 XX
 PS Claim 22; Page 59; 91pp; English.
 XX
 CC AAR95334-R95374 represent peptides derived from myelin basic protein
 CC (MBP). Immunisation with MBP can be used to induce experimental allergic
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+
 CC T-cell mediated autoimmune disease which results in demyelination of the
 CC central nervous system, resulting in paralysis and other neurological
 CC abnormalities. EAE is a commonly used animal model for human multiple
 CC sclerosis (MS). These sequences can be used in compositions for
 CC treating MS in a mammal. The composition acts to down regulate the
 CC autoimmune response, and may be administered in an amount sufficient to
 CC prevent the onset of symptoms of MS. The compositions may also be used
 CC to treat advanced stage MS, especially relapsing-remitting MS, chronic
 CC progressive MS or benign MS. These peptides may also be used in the
 CC treatment of other diseases involving myelin autoantigens, including
 CC diabetes, Graves disease, myasthenia gravis, Good Pasture's syndrome,
 CC psoriasis, thyroiditis, and rheumatoid arthritis. Peptides derived from
 CC other myelin autoantigens, such as myelin oligodendrocyte protein (MOG),
 CC proteolipid protein (PLP), and myelin associated glycoprotein (MAG) can
 CC be used as alternatives to these MBP peptides in these compositions.
 XX
 SQ Sequence 24 AA;

Query Match 49.2%; Score 128; DB 17; Length 24;
 Best Local Similarity 95.8%; Pred. No. 6.8e-10;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 22 DENPVVHFKNIVTPRTPPSQK 45
 DB 1 denpvvhfkniivtrtp 24

RESULT 26
 AAW50105
 ID AAW50105 standard; peptide; 24 AA.

XX AAW50105;

XX 30-JUN-1998 (first entry)

XX Pan DR binding peptide (2).

XX Pan DR binding peptide; antigen binding site; MHC molecule;
 KW DR locus.

XX Synthetic.

XX US5736142-A.

XX 07-APR-1998.

XX 14-SEP-1994; 94US-0305871.

XX 14-SEP-1994; 94US-0305871.

XX 14-SEP-1993; 93US-0121101.

XX (CYTE-) CYTEL CORP.

XX Alexander JL, Gaeta F, Grey HM, Sette A, Sidney J;
 XX WPI; 1998-239154/21.

XX Peptides that bind to MHC molecules of all DR alleles - inhibiting
 PT or inducing MHC Class II mediated activation of T cells
 XX
 PS Disclosure; Columns 31-32; 29pp; English.

XX The present sequence, a pan DR binding peptide, is capable of
 CC binding antigen binding sites on MHC molecules, which are encoded
 CC by most of the alleles of a DR locus. The peptide can be used to
 CC inhibit or induce MHC Class II mediated activation of T-cells or
 CC helper T-cells, which themselves mediate a CTL response. The
 CC peptide can be used in mammals, especially humans, to inhibit
 CC T-cell-mediated events involved in allograft rejection, allergic
 CC responses and autoimmunity and as a vaccine adjuvant for enhancing
 CC an immune response against an administered immunogen. The peptide
 CC can be used with other immunogens to treat, e.g. prostate cancer,
 CC hepatitis B, hepatitis C, AIDS, renal and cervical carcinoma,
 CC lymphoma, CMV and condyloma acuminatum.
 XX
 SQ Sequence 24 AA;

Query Match 49.2%; Score 128; DB 19; Length 24;
 Best Local Similarity 95.8%; Pred. No. 6.8e-10;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GRTQDENPVVHFFKNIVTPRTPPP 41
 ||||| ||||| ||||| ||||| |||||
 Db 1 grtqdenpvwhffknivtrtpppp 24

RESULT 27
 AAR95341
 ID AAR95341 standard; peptide: 21 AA.
 XX
 AC AAR95341;
 XX
 DT 16-DEC-1996 (first entry)
 XX
 DE MBP-2.4 (82-102).
 XX
 KW Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
 KW CD4+; T-cell; autoimmune disease; demyelination; central nervous system;
 KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;
 KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
 KW diabetes; Graves disease; myasthenia gravis; Good pasture's syndrome;
 KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
 KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
 XX
 OS Synthetic.
 XX
 PF WO9612737-A2.
 XX
 PD 02-MAY-1996.
 XX
 XX 25-OCT-1995; 95WO-US13682.
 XX
 XX 15-MAR-1995; 95US-0404228.
 PR 25-OCT-1994; 94US-0328224.
 PR 25-OCT-1995; 95ZA-0009033.
 XX
 PA (IMMU-) IMMULOGIC PHARM CORP.
 XX
 PI Devaux B, Franzen H, Geffer M, Hsu D, Palliard X;
 PI Rothbard J, Samson M, Shi J, Smillek D;
 XX
 XX WPI; 1996-230552/23.
 XX
 XX Myelin basic derived peptide(s) and analogs - used in the treatment
 PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.
 PT
 XX Claim 1; Fig 2; 91pp; English.
 PS
 XX AAR95334-R95374 represent peptides derived from myelin basic protein
 CC (MBP). Immunisation with MBP can be used to induce experimental allergic
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+
 CC T-cell mediated autoimmune disease which results in demyelination of the
 CC central nervous system, resulting in paralysis and other neurological

CC abnormalities. EAE is a commonly used animal model for human multiple
 CC sclerosis (MS). These sequences can be used in compositions for
 CC treating MS in a mammal. The composition acts to down regulate the
 CC autoimmune response, and may be administered in an amount sufficient to
 CC prevent the onset of symptoms of MS. The compositions may also be used
 CC to treat advanced stage MS, especially relapsing-remitting MS, chronic
 CC progressive MS or benign MS. These peptides may also be used in the
 CC treatment of other diseases involving myelin autoantigens, including
 CC diabetes, Graves disease, myasthenia gravis, Good pasture's syndrome,
 CC psoriasis, thyroiditis, and rheumatoid arthritis. Peptides derived from
 CC other myelin autoantigens, such as myelin oligodendrocyte protein (MOG),
 CC proteolipid protein (PLP), and myelin associated glycoprotein (MAG) can
 CC be used as alternatives to these MBP peptides in these compositions.
 XX
 SQ Sequence 21 AA;

Query Match 45.4%; Score 118; DB 17; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFFKNIVTPRTPPPS 42
 ||||| ||||| ||||| ||||| |||||
 Db 1 denpvvhffknivtrtpppps 21

RESULT 28
 AAW43947
 ID AAW43947 standard; peptide: 21 AA.
 XX
 AC AAW43947;
 XX
 DT 22-APR-1998 (first entry)
 XX
 DE Human myelin basic protein peptide MBP-2.4 (82-102).
 XX
 KW Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
 KW autoimmune response; MBP; myelin basic protein; demyelinating.
 XX
 OS Homo sapiens.
 XX
 PN WO9735879-A1.
 XX
 PD 02-OCT-1997.
 XX
 PF 01-MAY-1996; 96WO-US06072.
 XX
 PR 28-MAR-1996; 96US-0623406.
 XX
 PA (IMMU-) IMMULOGIC PHARM CORP.
 XX
 PI Devaux B, Garman RD, Rothbard J, Smillek D, Wallner B;
 XX
 XX WPI; 1997-489564/45.
 DR
 XX Human myelin oligodendrocyte glyco-protein peptide - useful to treat
 PT multiple sclerosis in mammal by down-regulating auto-immune response
 PT
 XX Claim 101; Page 35; 108pp; English.
 PS
 XX The present sequence represents a novel peptide of human myelin
 CC basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte
 CC glycoprotein) and MBP can be used to treat multiple sclerosis in a
 CC mammal by down-regulating an autoimmune response in the mammal. They
 CC can also be used to diagnose and treat other demyelinating autoimmune
 CC diseases in humans, or to prepare antibodies for the detection or
 CC diagnosis of autoimmune diseases.
 XX
 SQ Sequence 21 AA;

Query Match 45.4%; Score 118; DB 18; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e-08;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFFKNIVTPPTPPPS 42
Db 1 DENPVVHFFKNIVTPPTPPPS 21

RESULT 29
AAW10302
ID AAW10302 standard; peptide; 21 AA.

XX AC AAW10302;

XX DT 11-SEP-1997 (first entry)

XX DE Mammalian myelin basic peptide.

XX KW Soluble; fusion; major histocompatibility complex; MHC;
KW heterodimer; complex; MBP; antigen; binding groove; tolerance;
KW autoantigen; disease; insulin dependent; diabetes mellitus; IDDM;
KW antagonist; T cell; anergy; presenting cell; myelin basic peptide.

XX OS Mammalian spp.

XX PN W09640944-A2.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US10102.

XX PR 27-OCT-1995; 95US-0005964.

XX PR 07-JUN-1995; 95US-0480002.

XX PR 07-JUN-1995; 95US-0482133.

XX PR 07-JUN-1995; 95US-0483241.

XX PA (ANER-) ANERGEN INC.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Deshpande S, Gross JA, Kindvogel W, Reich EP, Sheppard PO;

XX WPI; 1997-052337/05.

XX Novel fused major histocompatibility complex-antigenic peptide
complex - useful to induce tolerance to an autoantigen-related
disease e.g. insulin-dependent diabetes mellitus

XX Claim 10; Page 107; 142pp; English.

XX A novel soluble fused major histocompatibility complex (MHC)
heterodimer; peptide complex, comprises DNA encoding 1st and 2nd
MHC domains, linked by DNA encoding a 5-25 residue linker, and a
DNA encoding an antigenic peptide able to associate with a peptide
binding groove of the MHC molecule, e.g. the present peptide,
linked in frame to the DNA encoding the 2nd domain by a DNA
encoding a 5-25 residue linker. The complex can be used to induce
immunological tolerance in adults susceptible to, or suffering from
an autoantigen related disease, e.g. insulin dependent diabetes
mellitus (IDDM), by antagonising the binding of particular T cells
and antigen presenting cells, to induce anergy (immunological
non-responsiveness) in the targeted T cell. As the heterodimers and
corresponding antigen are permanently linked into a single chain,
obviating the requirement for complex heterodimer truncation or
formation, the complex eliminates inefficient and non-specific
peptide loading.

XX Sequence 21 AA;

Query Match 45.4%; Score 118; DB 18; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.2e-08;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFFKNIVTPPTPPPS 42

Db 1 DENPVVHFFKNIVTPPTPPPS 21

RESULT 30

AAW54707
ID AAW54707 standard; peptide; 21 AA.

XX AC AAW54707;

XX DT 25-SEP-1998 (first entry)

XX DE Peptide from MBP (85-105).

XX KW Mannose; antigen; antigen-presenting cell; mannosylated peptide; T cell;
KW vaccine; treatment.

XX OS Synthetic.

XX PN W09813378-A1.

XX PD 02-APR-1998.

XX PF 25-SEP-1997; 97WO-NL00536.

XX PR 26-SEP-1996; 96EP-0202701.

XX PA (UYLE-) RIJKSUNIV LEIDEN.

XX PI Drijfhout JW, Koning F;

XX DR WPI; 1998-230631/20.

XX PT Increasing uptake and presentation of antigen(s) - by adding mannose
residue(s) to antigen for increasing T cell response, useful in,
e.g. vaccines against viral infection(s)

XX PS Disclosure; Page 32; 47pp; English.

XX The peptides AAW54559-W54809 are examples of peptides to which at least
1 (preferably 2) mannose can be attached to increase their uptake as
antigens by antigen-presenting cells. Uptake of agonist mannosylated
peptides will increase the T cell response, whereas uptake of antagonistic
peptides blocks the T cell response. Blocking binding of immunogenic
autoantigens can be used in treatment of type I diabetes, rheumatoid
arthritis, graft rejection etc., also to induce T-cell non-
responsiveness. Vaccines containing mannosylated antigen are used to
prevent or treat infections by, e.g. bacteria, viruses, fungi, helminths
and parasites.

XX Sequence 21 AA;

Query Match 45.0%; Score 117; DB 19; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.6e-08;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PVVHFFKNIVTPPTPPPSQK 45

Db 1 PVVHFFKNIVTPPTPPPSQK 21

RESULT 31

AAU69216
ID AAU69216 standard; Peptide; 21 AA.

XX AC AAU69216;

XX DT 29-JAN-2002 (first entry)

XX DE Human Myelin basic protein peptide MBP 85-105.

XX KW Human; epitope; autoimmune disease; myasthenia gravis;

KW Human leukocyte antigen; acetylcholine receptor; HLA DR3; HLA DR2; ACHR;
 KW antigen; immunosuppressive; major histocompatibility complex; MHC.

OS Homo sapiens.

PN W0200174848-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10450.

XX 31-MAR-2000; 2000US-193745P.

XX (CORI-) CORIXA CORP.

XX Deshpande S, Spack E, Wehner N, Arimilli S;

XX WPI; 2001-648547/74.

XX Peptide epitopes of the acetylcholine receptor target helper T cells
 PT recognize an antigen in association with an MHC component and are
 PT useful to treat autoimmune disease particularly myasthenia gravis

XX Example 1; Fig 4; 46pp; English.

XX The invention relates to a composition comprising an isolated
 CC acetylcholine receptor (AChR) oligopeptide of about 12 to 20 amino
 CC acids. The peptides form a set of 69 overlapping antigenic peptide
 CC epitopes which show various affinities for human leukocyte antigens
 CC (HLA) HLA-DR2 and DR3. Also included is a composition comprising an
 CC antigenic peptide and a major histocompatibility complex (MHC) component
 CC having an antigenic binding site, where binding of the peptide to
 CC the binding site induces non-responsiveness in a target T cell in a
 CC mammal, where the MHC component is an MHC class II component. Peptides
 CC with affinity for HLA-DR2 and DR3 from proteins other than AChR are also
 CC included. The composition is used to treat myasthenia gravis and other
 CC autoimmune diseases. The present sequence is an antigenic peptide
 CC epitope.

XX Sequence 21 AA;

Query Match 45.0%; Score 117; DB 22; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.6e-08;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PVVHFKNIVTPPTPPSQGK 45

Db 1 pvvhfknivtpptppsqgk 21

RESULT 32

AAR95350

ID AAR95350 standard; peptide; 20 AA.

XX AAR95350;

XX 16-DEC-1996 (first entry)

XX Residues 61-80 of myelin basic protein.

XX Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
 KW CD4+; T-cell; autoimmune disease; demyelination; central nervous system;
 KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;
 KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
 KW diabetes; graves disease; myasthenia gravis; Good Pasture's syndrome;
 KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
 KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.

OS Synthetic.

PN W09612737-A2.

PD 02-MAY-1996.

XX 25-OCT-1995; 95WO-US13682.

XX 15-MAR-1995; 95US-0404228.

XX 25-OCT-1994; 94US-0328224.

XX 25-OCT-1995; 95ZA-0009033.

XX (IMMU-) IMMULOGIC PHARM CORP.

XX Devaux B, Franzen H, Geffer M, Hsu D, Paliard X;

XX Rothbard J, Samson M, Shi J, Smilek D;

XX WPI; 1996-230552/23.

XX Myelin basic derived peptide(s) and analogs - used in the treatment

PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.

XX Claim 8; Fig 14; 91pp; English.

XX AAR95334-B95374 represent peptides derived from myelin basic protein
 CC (MBP). Immunisation with MBP can be used to induce experimental allergic
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+
 CC T-cell mediated autoimmune disease which results in demyelination of the
 CC central nervous system, resulting in paralysis and other neurological
 CC abnormalities. EAE is a commonly used animal model for human multiple
 CC sclerosis (MS). These sequences can be used in compositions for
 CC treating MS in a mammal. The composition acts to down regulate the
 CC autoimmune response, and may be administered in an amount sufficient to
 CC prevent the onset of symptoms of MS. The compositions may also be used
 CC to treat advanced stage MS, especially relapsing-remitting MS, chronic
 CC progressive MS or benign MS. These peptides may also be used in the
 CC treatment of other diseases involving myelin autoantigens, including
 CC diabetes, Graves disease, myasthenia gravis, Good Pasture's syndrome,
 CC psoriasis, thyroiditis, and rheumatoid arthritis. Peptides derived from
 CC other myelin autoantigens, such as myelin oligodendrocyte protein (MOG),
 CC proteolipid protein (PLP), and myelin associated glycoprotein (MAG) can
 CC be used as alternatives to these MBP peptides in these compositions.

XX Sequence 20 AA;

Query Match 44.2%; Score 115; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGLPQKSHGRT 20

Db 1 hhpatahygslpckshgrrt 20

RESULT 33

AAW44062

ID AAW44062 standard; peptide; 20 AA.

XX AAW44062;

XX 22-APR-1998 (first entry)

XX Human myelin basic protein peptide MBP-G (61-80).

XX Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
 KW autoimmune response; MBP; myelin basic protein; demyelinating.

OS Homo sapiens.

PN W09735879-A1.

XX 02-OCT-1997.

XX 01-MAY-1996; 96WO-US06072.

XX 28-MAR-1996; 96US-0623406.

XX PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX PI Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;
 XX XX WPI; 1997-489564/45.
 XX XX Human myelin oligodendrocyte glyco-protein peptide - useful to treat
 PT multiple sclerosis in mammal by down-regulating auto-immune response
 XX PS Disclosure; Page 35; 108pp; English.
 XX XX The present sequence represents a novel peptide of human myelin
 CC basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte
 CC glycoprotein) and MBP can be used to treat multiple sclerosis in a
 CC mammal by down-regulating an autoimmune response in the mammal. They
 CC can also be used to diagnose and treat other demyelinating autoimmune
 CC diseases in humans, or to prepare antibodies for the detection or
 CC diagnosis of autoimmune diseases.
 XX XX Sequence 20 AA;

Query Match 44.2%; Score 115; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYGSIPQKSHGRT 20
 DB 1 HHPARTAHYGSIPQKSHGRT 20

RESULT 34
 AAR46531
 ID AAR46531 standard; peptide; 24 AA.
 AC AAR46531;

DT 30-MAR-1994 (first entry)

DE Myelin basic protein sequence.

KW Autoimmunity; polar lipid; targeting; immune response; antigenic
 peptide; antigen.

OS Synthetic.

PN US5256641-A.

XX 26-OCT-1993.

XX 01-NOV-1990; 90US-0607982.

XX 09-JUL-1992; 92US-0911209.

XX (OREG-) STATE OF OREGON.

PA (UYOR-) UNIV OREGON HEALTH SCI.

XX PI Malkovsky M, Stowell MHB, Yatvin MB, Moclard RW;
 PI Parks DW, Wittefj;

DR WPI; 1993-350862/44.

XX New covalent conjugate of antigenic peptide and polar lipid e.g.
 PT sphingosine - useful in protective vaccines, treatment of
 PT auto-immune disease and preventing of transplant rejection

XX PS Disclosure; Page 13; 15pp; English.

XX CC The peptide is an example of an antigenic peptide which may be
 CC joined via a functional linker group, opt. at the two ends of a
 CC spacer group, to a polar lipid carrier, e.g. sphingosine, ceramide,
 CC phosphatidyl choline, ethanolamine, inositol or serine, cardiolipin

CC or phosphatidic acid. The compsn. may be used to alleviate
 CC autoimmune diseases. An advantage of the carrier system is that
 CC when incorporated into the compsn. entry of the antigenic peptide into
 CC the cells of the immune system is facilitated (no need for endocytosis)
 CC and targeting to specific organelles becomes possible. Unlike known
 CC vaccines, intracellular synthesis of viral antigens is not necessary
 CC for presentation via the MHC class I antigen pathway, nor intracellular
 CC proteolysis for presentation via the MHC class II antigen pathway, so
 CC both humoral and cellular immunity is achieved. Also, when a spacer is
 CC present, the antigen release rate may be controlled.
 CC See also AAR46507-47.

XX XX Sequence 24 AA;

Query Match 44.2%; Score 115; DB 14; Length 24;
 Best Local Similarity 91.7%; Pred. No. 3.4e-08;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 GRTODENPVVHFFKNIVPTPTPPP 41
 DB 1 grtqdenpvvhpknivptptppp 24

RESULT 35

AAR91923
 ID AAR91923 standard; peptide; 21 AA.

XX AAR91923;

DT 16-DEC-1996 (first entry)

DE Peptide comprising myelin basic protein residues 77-95.

KW Myelin basic protein MBP; neutralisation; modulation; production;
 antibody; treatment; multiple sclerosis.

OS Synthetic.

PN WO9612731-A1.

XX 02-MAY-1996.

XX 20-OCT-1995; 95WO-CA00583.

XX 21-OCT-1994; 94US-0327357.

XX (UYAL-) UNIV ALBERTA.

XX Catz I, Warren KG;

XX WPI; 1996-230547/23.

XX Peptide comprising residues 87-93 from myelin basic protein -
 PT modulates prodn. of anti-MBP antibodies and is useful for treating
 PT multiple sclerosis

XX Claim 6; Page 5; 53pp; English.

XX The present specifically claimed peptide, comprising residues 77-95
 CC of myelin basic protein (MBP), is capable of neutralising or
 CC modulating the prodn. of anti-MBP antibodies (Ab). The peptide can
 CC be used in a pharmaceutical compsn. for the treatment of multiple
 CC sclerosis (MS), administered i.v. at a dose of 1-10 mg/kg body wt.
 CC in a single or sequential dosage. Synthetically produced peptides
 CC unlike native MBP, prep. from human brain samples, are not
 CC potentially dangerous as they do not contain latent neuroviruses.
 CC Also MBP, which is not normally an immunogen, when administered to
 CC a patient may cause the prodn. of anti-MBP Ab increasing the risk
 CC of demyelination, however small synthetic peptides, due to their
 CC size, do not act as immunogens, but bind to anti-MBP Ab therefore
 CC modulating its effect. The peptide was prep. by standard solid
 CC phase synthesis, e.g. by the Fmoc method, and for admin. into the

CC CSF by means of lumbar puncture, it is dissolved in sterile normal
 CC saline. His F anti-MBP Ab levels were persistently elevated in a
 CC MS patient during a "time control" experiment or when 10 mg
 CC MBP35-58 was administered, however when 10 mg of the present
 CC peptide was injected, F anti-MBP Ab was completely neutralised and
 CC remained undetectable for 7 days.

XX Sequence 21 AA;

Query Match 43.8%; Score 114; DB 17; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4e-08;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KSHGRQTQDENPVVHFFKNIYV 35

DB 1 kshgrtqdenpvvwhffknivt 21

RESULT 36

AAW72359
 ID AAW72359 standard; peptide; 21 AA.

XX AAW72359;

DT 16-DEC-1998 (first entry)

XX Human myelin basic protein peptide MBP75-95.

DE Human; myelin basic protein; MBP; multiple sclerosis; anti-MBP; MS.

KW Homo sapiens.

OS W09845327-AL.

PN 15-OCT-1998.

XX 03-APR-1998; 98WO-CA00290.

XX 04-APR-1997; 97CA-2201841.

XX (UYAL-) UNIV ALBERTA.

PA Catz I, Warren KG;

PI WPI; 1998-568336/48.

DR Peptide and its derivatives for treatment of multiple sclerosis - is
 PT capable of neutralising or modulating production of anti-myelin
 PT basic protein

XX Claim 9; Page 47; 75pp; English.

XX The present sequence represents a myelin basic protein (MBP) peptide.
 CC The peptide is capable of neutralising or modulating the production of
 CC anti-myelin basic protein. The present invention also describes a method
 CC for treating multiple sclerosis (MS). The method comprises administering
 CC to the patient an MBP peptide of the formula:
 CC R1-Val-His-Phe-Phe-Lys-Asn-Ile-R2 where R1, R2 = H, OH, or an amino
 CC acid residue and a polypeptide residue, provided that R1 and R2 are not
 CC both H or OH at the same time.

XX Sequence 21 AA;

Query Match 43.8%; Score 114; DB 19; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4e-08;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 KSHGRQTQDENPVVHFFKNIYV 35

DB 1 kshgrtqdenpvvwhffknivt 21

RESULT 37

AAAR95392

ID AAR95392 standard; peptide; 20 AA.

XX AAR95392;

DT 16-DEC-1996 (first entry)

XX Residues 81-100 of myelin basic protein.

DE Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
 XX CD4+; T-cell; autoimmune disease; demyelination; central nervous system;
 XX CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;
 XX relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
 XX diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;
 XX psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
 XX myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.

OS Synthetic.

XX W09612737-A2.

XX 02-MAY-1996.

XX 25-OCT-1995; 95WO-US13682.

XX 15-MAR-1995; 95US-0404228.

XX 25-OCT-1994; 94US-0328224.

XX 25-OCT-1995; 95ZA-0009033.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.

XX Devaux B, Franzen H, Geffter M, Hsu D, Paliard X;

XX Rothbard J, Samson M, Shi J, Smillek D;

XX WPI; 1996-230552/23.

XX Myelin basic derived peptide(s) and analogs - used in the treatment
 of Multiple sclerosis, psoriasis, Graves Disease, etc.

XX Example 1; Fig 3; 9lpp; English.

XX AAR95334-R95374, and AAR95387-R95397 represent peptides derived from
 CC myelin basic protein (MBP). Immunisation with MBP can be used to induce
 CC experimental allergic encephalomyelitis (EAE) in susceptible strains of
 CC mice. EAE is a CD4+ T-cell mediated autoimmune disease which results in
 CC demyelination of the central nervous system, resulting in paralysis and
 CC other neurological abnormalities. EAE is a commonly used animal model
 CC for human multiple sclerosis (MS). These sequences can be used in
 CC compositions for treating MS in a mammal. The composition acts to down
 CC regulate the autoimmune response, and may be administered in an amount
 CC sufficient to prevent the onset of symptoms of MS. The compositions may
 CC also be used to treat advanced stage MS, especially relapsing-remitting
 CC MS, chronic progressive MS or benign MS. These peptides may also be
 CC used in the treatment of other diseases involving myelin autoantigens,
 CC including diabetes, Graves disease, myasthenia gravis, Good Pasture's
 CC syndrome, psoriasis, thyroiditis, and rheumatoid arthritis. Peptides
 CC derived from other myelin autoantigens, such as myelin oligodendrocyte
 CC protein (MOG), proteolipid protein (PLP), and myelin associated
 CC glycoprotein (MAG) can be used as alternatives to these MBP peptides in
 CC these compositions.

XX Sequence 20 AA;

Query Match 43.1%; Score 112; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QDENPVVHFFKNIYVPTPTTP 40

DB 1 qdenpvvwhffknivtrtp 20

RESULT 38

AAW34187
ID AAW34187 standard; peptide; 20 AA.

XX AC AAW34187;

XX DT 06-MAY-1998 (first entry)

XX DE Bt-MBP(83-102)083.

XX KW MHC class II molecule; major histocompatibility complex; T cell receptor;
 KW myelin basic protein; MBP; modified antigenic peptide; myasthenia gravis;
 KW rheumatoid arthritis; therapy; autoimmune disease; allograft rejection;
 KW systemic lupus erythematosus; insulin-dependent diabetes; cell typing;
 KW multiple sclerosis; allergy; autoreactive T cell.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Modified-site 1 /note= "biotinylated"

XX FT Misc-difference 1 /note= "mutated to Q"

XX FT Modified-site 20 /note= "C-terminal amide"

XX FT

XX PN WO9740852-AL.

XX PD 06-NOV-1997.

XX PF 18-MAR-1997; 97WO-US04360.

XX PR 30-APR-1996; 96US-0640344.

XX PA (ANER-) ANERGEN INC.

XX PI Deshpande S, Mukku P, Nag B;

XX DR WPI; 1997-549492/50.

XX PT Modified peptide antigen for major histocompatibility molecule -
 XX used specifically to inactivate T cell receptors implicated in
 XX auto-immune disease

XX PS Example; Page 25; 45pp; English.

XX CC This sequence represents a modified fragment of the myelin basic protein
 CC (MBP). This sequence can be used in the modified antigenic peptide of the
 CC invention. The modified antigenic peptide (A) is for a major
 CC histocompatibility complex (MHC) class II molecule, and has the amino
 CC acid structure Y-Z, where Y = a hydrophobic amino acid (aa), or a series
 CC of 1-5 aa of which at least one is hydrophobic; and Z = a peptide epitope
 CC for the MHC class II molecule. (A) has a higher affinity for the MHC
 CC class II molecule than the peptide epitope. When a complex containing (A)
 CC can bind to, and inactivate, a T cell receptor it is useful for
 CC preventing or treating disorders associated with autoreactive T cells,
 CC particularly autoimmune diseases, specifically rheumatoid arthritis (RA),
 CC systemic lupus erythematosus (SLE), insulin-dependent diabetes,
 CC myasthenia gravis (MG) and multiple sclerosis (MS). The complex
 CC containing (A) can also be used for preventing or treating allergy and
 CC allograft rejection. The complex can be used to detect specific
 CC autoreactive T cells, from their ability to bind to the complex. The
 CC complex can also be used for in vivo/in vitro diagnosis, including T cell
 CC typing, isolation or labelling of specific cells, to assay potential
 CC inhibitors of MHC cell interactions, for imaging and monitoring
 CC treatment. Addition of Y improves bonding, probably by providing an
 CC anchor within the MHC antigen-binding pocket, and thus provides higher
 CC occupancy of this pocket.

XX SQ Sequence 20 AA;

Query Match 43.1%; Score 112; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QDENPVVHFFKNIVTPRTPP 40

DB 1 QDENPVVHFFKNIVTPRTPP 20

RESULT 39

AAW44064

ID AAW44064 standard; peptide; 20 AA.

XX AC AAW44064;

XX DT 22-APR-1998 (first entry)

XX DE Human myelin basic protein peptide MBP-I (81-100).

XX KW Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
 KW autoimmune response; MBP; myelin basic protein; demyelinating.

XX OS Homo sapiens.

XX PN WO9735879-AL.

XX PD 02-OCT-1997.

XX PF 01-MAY-1996; 96WO-US06072.

XX PR 28-MAR-1996; 96US-0623406.

XX PA (TMOU-) IMMULOGIC PHARM CORP.

XX PI Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;

XX DR WPI; 1997-489564/45.

XX PT Human myelin oligodendrocyte glyco-protein peptide - useful to treat
 XX multiple sclerosis in mammal by down-regulating auto-immune response

XX PS Disclosure; Page 35; 108pp; English.

XX CC The present sequence represents a novel peptide of human myelin
 CC basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte
 CC glycoprotein) and MBP can be used to treat multiple sclerosis in a
 CC mammal by down-regulating an autoimmune response in the mammal. They
 CC can also be used to diagnose and treat other demyelinating autoimmune
 CC diseases in humans, or to prepare antibodies for the detection or
 CC diagnosis of autoimmune diseases.

XX SQ Sequence 20 AA;

Query Match 43.1%; Score 112; DB 18; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.9e-08;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QDENPVVHFFKNIVTPRTPP 40

DB 1 QDENPVVHFFKNIVTPRTPP 20

RESULT 40

AAB26882

ID AAB26882 standard; peptide; 20 AA.

XX AC AAB26882;

XX DT 01-FEB-2001 (first entry)

XX DE Murine myelin basic protein fragment.

XX Immunosuppressant; neuroprotective; multiple sclerosis; treatment.
 KW Mus sp.
 XX WO200058654-A1.
 OS 05-OCT-2000.
 PN 29-MAR-1999; 99WO-EP02268.
 XX 29-MAR-1999; 99WO-EP02268.
 PD (TECN-) TECHNOGEN SCPA.
 XX Marino M, Ippolito A, Fassina G;
 PI WPI; 2000-628344/60.
 XX New glycine-rich peptides, useful for treatment of multiple sclerosis
 DR by induction of energy in autoreactive T cells -
 PT Example 1; Page 10; 23pp; English.
 PS Peptides AAB26878-B26881 represent four glycine rich peptide which may
 XX be N-acetylated and/or C-aminated and contain amino acids with L or D
 CC configuration. Included in the invention is a pharmaceutical composition
 CC containing at least one of the peptides and an inert ingredient. The
 CC peptides have immunosuppressant and neuroprotective activity and induce
 CC response of autoreactive T lymphocytes without inducing an autoreactive
 CC response. The peptides are used to treat multiple sclerosis. The present
 CC sequence represents a fragment of the murine myelin basic protein which
 CC is used as a comparison peptide when testing the effectiveness of the
 CC peptides of the invention.
 XX Sequence 20 AA:
 SQ

Query Match 43.1%; Score 112; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 6.9e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 NPVVHFFKNIVTPRTPPPSQ 43
 IIIIIIIIIIIIIIIIIIII
 Db 1 npvvhffknivtrtppps q 20

RESULT 41
 AAR95391
 ID AAR95391 standard; peptide; 20 AA.
 XX AAR95391;
 AC 16-DEC-1996 (first entry)
 DT Residues 71-90 of myelin basic protein.
 DE
 XX Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
 KW CD4+; T-cell; autoimmune disease; demyelination; central nervous system;
 KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;
 KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
 KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;
 KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
 KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
 XX Synthetic.
 OS WO9612737-A2.
 PN 02-MAY-1996.
 XX 02-MAY-1996.
 PD 25-OCT-1995; 95WO-US13682.
 XX

15-MAR-1995; 95US-0404228.
 25-OCT-1994; 94US-0328224.
 25-OCT-1995; 95ZA-0009033.
 XX (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX Devaux B, Franzen H, Geffer M, Hsu D, Pallard X;
 PI Rothbard J, Samson M, Shi J, Smilek D;
 PI WPI; 1996-230352/23.
 DR Myelin basic derived peptide(s) and analogs - used in the treatment
 XX of Multiple Sclerosis, psoriasis, Graves Disease, etc.
 PS Example 1; Fig 3; 9pp; English.
 XX AAR95334-R95374, and AAR95387-R95397 represent peptides derived from
 CC myelin basic protein (MBP). Immunisation with MBP can be used to induce
 CC experimental allergic encephalomyelitis (EAE) in susceptible strains of
 CC mice. EAE is a CD4+ T-cell mediated autoimmune disease which results in
 CC demyelination of the central nervous system, resulting in paralysis and
 CC other neurological abnormalities. EAE is a commonly used animal model
 CC for human multiple sclerosis (MS). These sequences can be used in
 CC compositions for treating MS in a mammal. The composition acts to down
 CC regulate the autoimmune response, and may be administered in an amount
 CC sufficient to prevent the onset of symptoms of MS. The compositions may
 CC also be used to treat advanced stage MS, especially relapsing-remitting
 CC MS, chronic progressive MS or benign MS. These peptides may also be
 CC used in the treatment of other diseases involving myelin autoantigens,
 CC including diabetes, Graves disease, myasthenia gravis, Good Pasture's
 CC syndrome, psoriasis, thyroiditis, and rheumatoid arthritis. Peptides
 CC derived from other myelin autoantigens, such as myelin oligodendrocyte
 CC protein (MOG), proteolipid protein (PLP), and myelin associated
 CC glycoprotein (MAG) can be used as alternatives to these MBP peptides in
 CC these compositions.
 XX Sequence 20 AA:
 SQ

Query Match 42.3%; Score 110; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 1.3e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLPQKSHGRTQDENPVVHFF 30
 IIIIIIIIIIIIIIIIIIII
 Db 1 slpqkshgtrtdenpvvhff 20

RESULT 42
 AAR95362
 ID AAR95362 standard; peptide; 20 AA.
 XX AAR95362;
 AC 16-DEC-1995 (first entry)
 DT Residues 86-105 of myelin basic protein.
 DE
 XX Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
 KW CD4+; T-cell; autoimmune disease; demyelination; central nervous system;
 KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;
 KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
 KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;
 KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
 KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
 XX Synthetic.
 OS WO9612737-A2.
 PN 02-MAY-1996.
 XX 02-MAY-1996.
 PD 25-OCT-1995; 95WO-US13682.
 XX

XX 15-MAR-1995; 95US-0404228.
 PR 25-OCT-1994; 94US-0328224.
 PR 25-OCT-1995; 95ZA-0009033.
 XX (IMMU-) IMMULOGIC PHARM CORP.
 PA Devaux B, Franzen H, Geffer M, Hsu D, Pallard X;
 PI Rothbard J, Samson M, Shi J, Smilek D;
 XX WPI; 1996-230552/23.
 DR Myelin basic derived peptide(s) and analogs - used in the treatment
 PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.
 PT Claim 8; Fig 14; 51pp; English.
 XX AAR95334-R95374 represent peptides derived from myelin basic protein
 CC (MBP). Immunisation with MBP can be used to induce experimental allergic
 CC encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+
 CC T-cell mediated autoimmune disease which results in demyelination of the
 CC central nervous system, resulting in paralysis and other neurological
 CC abnormalities. EAE is a commonly used animal model for human multiple
 CC sclerosis (MS). These sequences can be used in compositions for
 CC treating MS in a mammal. The composition acts to down regulate the
 CC autoimmune response, and may be administered in an amount sufficient to
 CC prevent the onset of symptoms of MS. The compositions may also be used
 CC to treat advanced stage MS, especially relapsing-remitting MS, chronic
 CC progressive MS or benign MS. These peptides may also be used in the
 CC treatment of other diseases involving myelin autoantigens, including
 CC diabetes, Graves disease, myasthenia gravis, Good Pasture's syndrome,
 CC psoriasis, thyroiditis, and rheumatoid arthritis. Peptides derived from
 CC other myelin autoantigens, such as myelin oligodendrocyte protein (MOG),
 CC proteolipid protein (PLP), and myelin associated glycoprotein (MAG) can
 CC be used as alternatives to these MBP peptides in these compositions.
 XX Sequence 20 AA;
 SQ

Query Match 42.3%; Score 110; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 VVHFKNIVTRTPPPSQGK 45
 |||||
 Db 1 vvhfknivtrtppps gk 20

RESULT 43
 AAW44063
 ID AAW44063 standard; peptide; 20 AA.
 XX AAW44063;
 XX 22-APR-1998 (first entry)
 DT Human myelin basic protein peptide MBP-H (71-90).
 DE Human myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis;
 KW autoimmune response; MBP; myelin basic protein; demyelinating.
 KW Homo sapiens.
 OS WO9735879-1.
 PN 02-OCT-1997.
 PD 01-MAY-1996; 96WO-US06072.
 PF 28-MAR-1996; 95US-0623406.
 PR (IMMU-) IMMULOGIC PHARM CORP.
 PA

PI Devaux B, Garman RD, Rothbard J, Smilek D, Wallner B;
 XX WPI; 1997(489564/45.
 DR Human myelin oligodendrocyte glyco-protein peptide - useful to treat
 PT multiple sclerosis in mammal by down-regulating auto-immune response
 XX Disclosure; Page 35; 108pp; English.
 XX The present sequence represents a novel peptide of human myelin
 CC basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte
 CC glycoprotein) and MBP can be used to treat multiple sclerosis in a
 CC mammal by down-regulating an autoimmune response in the mammal. They
 CC can also be used to diagnose and treat other demyelinating autoimmune
 CC diseases in humans or to prepare antibodies for the detection or
 CC diagnosis of autoimmune diseases.
 XX Sequence 20 AA;
 SQ

Query Match 42.3%; Score 110; DB 18; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SLPOKSHGRTQDENPVVHFF 30
 |||||
 Db 1 slpqkshgrtqdenpvvhff 20

RESULT 44
 AAB33636
 ID AAB33636 standard; Peptide; 20 AA.
 XX AAB33636;
 XX 26-JAN-2001 (first entry)
 DT MHC class II associated immunogenic peptide SEQ ID 35.
 DE Microparticle; nucleic acid delivery; immunogenic peptide; MHC I; MHC II;
 KW major histocompatibility complex; vaginal tissue; mucosal tissue...
 XX Unidentified.
 OS WO2000053061-A2.
 PN 14-SEP-2000.
 PD 10-MAR-2000; 2000WO-US06578.
 PF 11-MAR-1999; 99US-0266463.
 PR 27-MAY-1999; 99US-0321346.
 XX (ZYCO-) ZYCOS INC.
 PA Lunsford LB, Pugham D, Hedley ML;
 PI WPI; 2000-638130/6.
 DR Microparticles useful for administering a nucleic acid into the mucosal
 PT tissue preferably vaginal tissue of an animal, comprises a polymeric
 PT matrix, a lipid and a nucleic acid molecule -
 XX Claim 25; Page 11; 96pp; English.
 XX The present invention relates to microparticles which are less than 20
 CC microns in diameter, which comprise a polymeric matrix, a lipid and a
 CC nucleic acid molecule. The microparticle is specifically not
 CC encapsulated in a liposome and does not comprise a cell. The nucleotide
 CC sequence encodes an expression product that binds to major
 CC histocompatibility complex (MHC) type I or II molecules. Peptides
 CC AAB33602-B33647 represent MHC class II associated immunogenic peptides,
 CC and AAB33648-B33710 represent MHC class I associated immunogenic

CC peptides. The peptides are examples of the expression products of the
CC nucleotide sequences which can be included in the microparticles of the
CC invention. Sequences AAB33711-B33716 represent alternative expression
CC products and nuclear localisation signals also used in the invention. The
CC microparticles are useful for administering a nucleic acid into the
CC mucosal tissue preferably vaginal tissue of an animal.

XX Sequence 20 AA;

Query Match 42.3%; Score 110; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 QKSHGRTQDENPVVHFFKNI 33
Db 1 qkshgrtqdenpvvhffknl 20

RESULT 45

AAG93732
ID AAG93732 standard; Peptide; 20 AA.

XX AAG93732;

AC AAG93732;

DT 17-SEP-2001 (first entry)

DE Human myelin basic protein peptide 4.
XX Continuous flow production; microparticle; gene therapy;
KW antisense therapy; vaccination; treatment; autoimmune disease;
KW immune response modulation.

XX Homo sapiens

OS WO200136583-A1.

PN 25-MAY-2001.

PD 17-NOV-2000; 2000WO-US31770.

PF 19-NOV-1999; 99US-0443654.

PR (ZYCO-) ZYCO INC.

XX Hedley ML, Hsu Y, Tyo M;

PI WPI; 2001-425203/45.

DR Continuous production of microparticles containing nucleic acid for
XX e.g. gene therapy, comprises mixing a solution of polymeric material
PT and nucleic acid with a surfactant solution, removing solvent and
PT drying -

XX Disclosure; Page 9; 47pp; English.

XX The present sequence is that of a peptide of the invention.
XX The invention relates to a method for scalable, continuous flow
CC production of a nucleic acid containing microparticle that maintains the
CC structural integrity of the associated nucleic acid and results in a
CC microparticle having purity suitable for introduction into an animal
CC host. Microparticles prepared according to the method can be used for
CC delivery of a nucleic acid for gene therapy, antisense therapy,
CC vaccination, treatment of autoimmune disease and either specific or
CC non-specific modulation of an immune response. The microparticles may
CC also be used to deliver nucleic acid encoding a protein or peptide useful
CC in any kind of therapy. The method is economical, aseptic and scalable.
CC The method also enables control over the size of microparticles. The
CC microparticles produced are free of impurities such as organic solvents
CC and are readily dispersed in a wide range of dispersing agents.

XX Sequence 20 AA;

Query Match 42.3%; Score 110; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 QKSHGRTQDENPVVHFFKNI 33
Db 1 qkshgrtqdenpvvhffknl 20

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Job time: 83 sec

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OM protein - protein search, using sw model

Run on: September 23, 2002, 11:08:56 ; Search time 12.84 Seconds
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Title: US-09-813-383-1

Perfect score: 260

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Total number of hits satisfying chosen parameters: 138714

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Maximum DB seq length: 27

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135	51.9	24	2	US-08-480-190-46
2	135	51.9	24	2	US-08-488-379-46
3	135	51.9	24	5	PCT-US93-07545-46
4	128	49.2	23	1	US-08-787-547-1
5	128	49.2	24	1	US-08-305-871A-2
6	113	44.2	20	3	US-08-297-395-20
7	112	43.1	20	2	US-08-640-344-6
8	110	42.3	20	1	US-08-787-547-35
9	110	42.3	20	3	US-08-297-395-21
10	108	41.5	20	2	US-08-640-344-4
11	107	41.2	19	2	US-08-640-344-2
12	107	41.2	19	2	US-08-468-540B-9
13	107	41.2	19	3	US-08-297-395-1
14	107	41.2	19	4	US-09-024-220-2
15	107	41.2	19	4	US-08-960-190A-32
16	107	41.2	19	4	US-08-449-728-2
17	107	41.2	20	2	US-08-640-344-1
18	107	41.2	20	2	US-08-640-344-3
19	107	41.2	20	2	US-08-640-344-5
20	107	41.2	20	2	US-08-640-344-7
21	107	41.2	20	2	US-08-468-540B-7
22	107	41.2	20	4	US-08-960-190A-28
23	103.5	39.8	26	1	US-08-227-372-2
24	103.5	39.8	26	3	US-08-470-397-2
25	102	39.2	20	1	US-08-227-372-3
26	102	39.2	20	2	US-08-468-540B-8
27	102	39.2	20	3	US-08-470-397-3

Sequence 18, Appl
Sequence 17, Appl
Sequence 24, Appl
Sequence 19, Appl
Sequence 3, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 10, Appl
Sequence 22, Appl
Sequence 30, Appl
Sequence 22, Appl
Sequence 37, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 23, Appl
Sequence 36, Appl
Sequence 3, Appl

28 101 38.8 18 2 US-08-468-540B-18
29 100 38.5 19 2 US-08-468-540B-17
30 100 38.5 19 2 US-08-468-540B-24
31 96 36.9 17 2 US-08-468-540B-19
32 94 36.2 17 4 US-09-137-759-3
33 93 35.8 17 2 US-08-468-540B-20
34 88 33.8 16 2 US-08-468-540B-21
35 88 33.8 20 2 US-08-468-540B-10
36 88 33.8 20 3 US-08-297-395-22
37 85.5 32.9 19 4 US-09-153-586-30
38 83 31.9 15 2 US-08-468-540B-22
39 82 31.5 15 1 US-08-787-547-37
40 82 31.5 15 2 US-08-468-540B-16
41 82 31.5 15 2 US-08-400-796-16
42 81.5 31.3 19 4 US-09-153-586-25
43 77 29.5 14 2 US-08-468-540B-23
44 76 29.2 14 1 US-08-787-547-36
45 76 29.2 14 4 US-08-342-408B-3

ALIGNMENTS

RESULT 1
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; Sequence 46, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

US-08-480-190-46

100

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-1

Query Match 49.2%; Score 128; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 8.2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GRTQDENPVVHFFKNIVTPRTPP 40
DB 1 GRTQDENPVVHFFKNIVTPRTPP 23

RESULT 5

US-08-305-871A-2
Sequence 2, Application US/08305871A
Patent No. 5736142
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Gaeta, Federico
APPLICANT: Grey, Howard M.
APPLICANT: Sidney, John
APPLICANT: Alexander, Jeffrey L.
TITLE OF INVENTION: Alteration of Immune Response Using Pan
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/305,871A
FILING DATE: 14-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 08/121,101
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-0062-10

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-305-871A-2

Query Match 49.2%; Score 128; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 8.6e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GRTQDENPVVHFFKNIVTPRTPP 41
DB 1 GRTQDENPVVHFFKNIVTPRTPP 24

RESULT 6

US-08-297-395-20
Sequence 20, Application US/08297395A
Patent No. 6039947
GENERAL INFORMATION:
APPLICANT: Howard L. Weiner
APPLICANT: David A. Hafler
TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
TITLE OF INVENTION: EPITOPES OF MYELIN BASIC PROTEIN
FILE REFERENCE: 1010/057230S3
CURRENT APPLICATION NUMBER: US/08/297,395A
CURRENT FILING DATE: 1994-08-11
EARLIER APPLICATION NUMBER: 08/059,189
EARLIER FILING DATE: 1993-05-06
EARLIER APPLICATION NUMBER: 07/502,559
EARLIER FILING DATE: 1990-03-30
EARLIER APPLICATION NUMBER: PCT/US88/02139
EARLIER FILING DATE: 1988-06-24
EARLIER APPLICATION NUMBER: 07/065,734
EARLIER FILING DATE: 1987-06-24
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 20
TYPE: PPT
ORGANISM: Homo sapiens
US-08-297-395-20

Query Match 44.2%; Score 115; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHPARTAHYCSLPQKSHGRT 20
DB 1 HHPARTAHYCSLPQKSHGRT 20

RESULT 7

US-08-640-344-6
Sequence 6, Application US/08640344
Patent No. 5824315
GENERAL INFORMATION:
APPLICANT: NAG, BISHWAJIT
APPLICANT: MUKKU, PRABHA
APPLICANT: DESHPANDE, SHRIKANT
TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
TITLE OF INVENTION: PEPTIDES FOR MHC MOLECULES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP

STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,344
FILING DATE: 30-APR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STORELIA ESQ., JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 14058-004800
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-640-344-6

Query Match 43.1%; Score 112; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 QDENPVHFEKNIIVTPTTP 40
Db 1 QDENPVHFEKNIIVTPTTP 20

RESULT 8
US-08-787-547-35
Sequence 35, Application US/08787547
Patent No. 5783567
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Langer, Joanne M.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-35

Query Match 42.3%; Score 110; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 QKSHGRTQDENPVVHFFKNI 33
Db 1 QKSHGRTQDENPVVHFFKNI 20

RESULT 9
US-08-297-395-21
Sequence 21, Application US/08297395A
Patent No. 6039947
GENERAL INFORMATION:
APPLICANT: Howard L. Weiner
APPLICANT: David A. Hafler
TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
EPITOPES OF MYELIN BASIC PROTEIN
FILE REFERENCE: 1010/05723US3
CURRENT APPLICATION NUMBER: US/08/297,395A
CURRENT FILING DATE: 1994-08-11
EARLIER APPLICATION NUMBER: 08/059,189
EARLIER FILING DATE: 1993-05-06
EARLIER APPLICATION NUMBER: 07/502,559
EARLIER FILING DATE: 1990-03-30
EARLIER APPLICATION NUMBER: PCT/US88/02139
EARLIER FILING DATE: 1988-06-24
EARLIER APPLICATION NUMBER: 07/065,734
EARLIER FILING DATE: 1987-06-24
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 20
TYPE: PPT
ORGANISM: Homo sapiens
US-08-297-395-21

Query Match 42.3%; Score 110; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 SLPKSHGRTQDENPVVHFF 30
Db 1 SLPKSHGRTQDENPVVHFF 20

RESULT 10
US-08-640-344-4
Sequence 4, Application US/08640344
Patent No. 5824315
GENERAL INFORMATION:
APPLICANT: NAG, BISHWAJIT
APPLICANT: MUKU, PRABHA
APPLICANT: DESHPANDE, SHRIKANT
TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
PEPTIDES FOR MHC MOLECULES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 30-APR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA ESQ., JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 14058-004800
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-640-344-4

Query Match 41.5%; Score 108; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.2e-08;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 21 QDENPVVHFFKNIVTPRTPP 40
Db 1 KDENPVVHFFKNIVTPRTPP 20

RESULT 11
US-08-640-344-2
; Sequence 2, Application US/08640344
; Patent No. 5824315
; GENERAL INFORMATION:
; APPLICANT: NAG, BISHWALIT
; APPLICANT: MUKU, PRABHA
; APPLICANT: DESHPANDE, SHRIRANT
; TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
; TITLE OF INVENTION: PEPTIDES FOR MHC MOLECULES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,344
; FILING DATE: 30-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STORELLA ESQ., JOHN R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 14058-004800
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-640-344-2

Query Match 41.2%; Score 107; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 DENPVVHFFKNIVTPRTPP 40
Db 1 DENPVVHFFKNIVTPRTPP 19

RESULT 12
US-08-468-540B-9
; Sequence 9, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafler, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
US-08-468-540B-9

Query Match 41.2%; Score 107; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFKNIVTPRTP 40
 DB 1 DENPVVHFKNIVTPRTP 19

RESULT 13

US-08-297-395-1
 ; Sequence 1, Application US/08297395A
 ; Patent No. 6039947
 ; GENERAL INFORMATION:
 ; APPLICANT: Howard L. Weiner
 ; APPLICANT: David A. Hafler
 ; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
 ; FILE OF INVENTION: EPTIDES OF MYELIN BASIC PROTEIN
 ; FILE REFERENCE: 1010/05723US3
 ; CURRENT APPLICATION NUMBER: US/08/297,395A
 ; CURRENT FILING DATE: 1994-08-11
 ; EARLIER APPLICATION NUMBER: 08/059,189
 ; EARLIER FILING DATE: 1993-05-06
 ; EARLIER APPLICATION NUMBER: 07/502,559
 ; EARLIER FILING DATE: 1990-03-30
 ; EARLIER APPLICATION NUMBER: PCT/US88/02139
 ; EARLIER FILING DATE: 1988-06-24
 ; EARLIER APPLICATION NUMBER: 07/065,734
 ; EARLIER FILING DATE: 1987-06-24
 ; NUMBER OF SEQ ID NOS: 84
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-08-297-395-1

Query Match 41.2%; Score 107; DB 3; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.1e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFKNIVTPRTP 40
 DB 1 DENPVVHFKNIVTPRTP 19

RESULT 14

US-09-024-220-2
 ; Sequence 2, Application US/09024220
 ; Patent No. 6197311
 ; GENERAL INFORMATION:
 ; APPLICANT: RAYCHAUDHURI, Syamal
 ; RASTETTER, William H.
 ; BLACK, Amelia
 ; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC T-LYMPHOCYTE
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/024,220
 ; FILING DATE: 17-Feb-1998
 ; CLASSIFICATION: <Unknown>
 ; 24-JUL-1992
 ; 25-JUL-1991

;; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/476,674
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 07/919,787
 ; FILING DATE: 24-JUL-1992
 ; APPLICATION NUMBER: US 07/735,069
 ; FILING DATE: 25-JUL-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Teskin, Robin L.
 ; REGISTRATION NUMBER: 35,030
 ; REFERENCE/DOCKET NUMBER: 012712-149
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-024-220-2

Query Match 41.2%; Score 107; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.1e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFKNIVTPRTP 40
 DB 1 DENPVVHFKNIVTPRTP 19

RESULT 15

US-08-960-190A-32
 ; Sequence 32, Application US/08960190A
 ; Patent No. 6232445
 ; GENERAL INFORMATION:
 ; APPLICANT: Rhode, Peter R.
 ; APPLICANT: Acevedo, Jorge
 ; APPLICANT: Burkhardt, Martin
 ; APPLICANT: Jiao, Jin-an
 ; APPLICANT: Wong, Hing C.
 ; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
 ; METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: usa
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/960,190A
 ; FILING DATE: 29-OCT-1997
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Corless, Peter F.
 ; REGISTRATION NUMBER: 33,860
 ; REFERENCE/DOCKET NUMBER: 48002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-523-3400
 ; TELEFAX: 617-523-6440

TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-960-190A-32

Query Match 41.2%; Score 107; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFFKNIIVTPRTPP 40
| | | | | | | | | | | | | | | | | | | | | |
DB 1 DENPVVHFFKNIIVTPRTPP 19

RESULT 16
US-08-449-728-2
; Sequence 2, Application US/08449728
; Patent No. 6270769
; GENERAL INFORMATION:
; APPLICANT: SYAMAL RAYCHAUDHURI
; APPLICANT: WILLIAM H. RASTETTER
; TITLE OF INVENTION: INDUCTION OF CYTOTOXIC
; TITLE OF INVENTION: T-LYMPHOCYTE RESPONSES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,728
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/735,069
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 194/160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-449-728-2

Query Match 41.2%; Score 107; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFFKNIIVTPRTPP 40
| | | | | | | | | | | | | | | | | | | | | |
DB 1 DENPVVHFFKNIIVTPRTPP 19

RESULT 17
US-08-640-344-1
; Sequence 1, Application US/08640344
; Patent No. 5824315
; GENERAL INFORMATION:
; APPLICANT: NAG, BISHWAJIT
; APPLICANT: MUKKU, PRABHA
; APPLICANT: DESHPANDE, SHRIRAKT
; TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
; TITLE OF INVENTION: PEPTIDES FOR MHC MOLECULES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,344
; FILING DATE: 30-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STORELLA ESQ., JOHN R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 14058-004800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-640-344-1

Query Match 41.2%; Score 107; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFFKNIIVTPRTPP 40
| | | | | | | | | | | | | | | | | | | | | |
DB 2 DENPVVHFFKNIIVTPRTPP 20

RESULT 18
US-08-640-344-3
; Sequence 3, Application US/08640344
; Patent No. 5824315
; GENERAL INFORMATION:
; APPLICANT: NAG, BISHWAJIT
; APPLICANT: MUKKU, PRABHA
; APPLICANT: DESHPANDE, SHRIRAKT
; TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
; TITLE OF INVENTION: PEPTIDES FOR MHC MOLECULES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,344
FILING DATE: 30-APR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA ESQ., JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 14058-004800
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-640-344-3

Query Match 41.2%; Score 107; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFFKNIIVTPRTPP 40
Db 2 DENPVVHFFKNIIVTPRTPP 20
|||||

RESULT 19
US-08-640-344-5
Sequence 5, Application US/08640344
Patent No. 5824315
GENERAL INFORMATION:
APPLICANT: NAG, BISHWAJIT
APPLICANT: MUKKU, PRABHA
APPLICANT: DESHPANDE, SHRIKANT
TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
MOLECULES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,344
FILING DATE: 30-APR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA ESQ., JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 14058-004800
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-640-344-5

Query Match 41.2%; Score 107; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFFKNIIVTPRTPP 40
Db 2 DENPVVHFFKNIIVTPRTPP 20
|||||

RESULT 20
US-08-640-344-7
Sequence 7, Application US/08640344
Patent No. 5824315
GENERAL INFORMATION:
APPLICANT: NAG, BISHWAJIT
APPLICANT: MUKKU, PRABHA
APPLICANT: DESHPANDE, SHRIKANT
TITLE OF INVENTION: IMPROVING BINDING AFFINITY OF ANTIGENIC
MOLECULES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,344
FILING DATE: 30-APR-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STORELLA ESQ., JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 14058-004800
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-640-344-7

Query Match 41.2%; Score 107; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFFKNIIVTPRTPP 40
Db 2 DENPVVHFFKNIIVTPRTPP 20
|||||

RESULT 21
US-08-468-540B-7
Sequence 7, Application US/08468540B
Patent No. 5858980
GENERAL INFORMATION:

APPLICANT: Weiner, Howard
APPLICANT: Hafner, David
APPLICANT: Miller, Ariel
APPLICANT: Al-Sabbagh, Ahmed
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,540B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32,140
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5858980e
US-08-468-540B-7

Query Match 41.2%; Score 107; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HHPARTAHYGSLPQKSHGRT 20
Db 1 HHPARTAHYGSLPQKSEGT 20

RESULT 22
US-08-960-190A-28
Sequence 28, Application US/08960190A
Patent No. 6232445
GENERAL INFORMATION:
APPLICANT: Rhode, Peter R.
APPLICANT: Acevedo, Jorge
APPLICANT: Burkhardt, Martin
APPLICANT: Jiao, Jin-an
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: usa
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,190A
FILING DATE: 29-OCT-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 48002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-960-190A-28

Query Match 41.2%; Score 107; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFKNIVTPRTPP 40
Db 2 DENPVVHFKNIVTPRTPP 20

RESULT 23
US-08-227-372-2
Sequence 2, Application US/08227372
Patent No. 5763585
GENERAL INFORMATION:
APPLICANT: Nag, Bishwajit
TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF
TITLE OF INVENTION: MHC-PEPTIDE COMPLEXES USEFUL IN AMELIORATING AUTOIMMUNITY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,372
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136,216
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14058-32-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600

[illegible]

ADDRESS: Darby & Darby P. O.

STREET: 805 Third Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,540B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32,140
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5858980e
US-08-468-540B-8

Query Match 39.2%; Score 102; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 2e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 SLPOKSHGRTQDENPVVHFF 30
Db 1 SLPOKSEGTQDENPVVHFF 20

RESULT 27
US-08-470-397-3
Sequence 3, Application US/08470397
Patent No. 6007820
GENERAL INFORMATION:
APPLICANT: Nag, Bishwajit
TITLE OF INVENTION: Purification and Characterization of
TITLE OF INVENTION: MHC-Peptide Complexes Useful in Ameliorating Autoimmunity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower, 20th
FLOOR
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,397
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136,216
FILING DATE: 13-OCT-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,372
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14058-32-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-470-397-3

Query Match 39.2%; Score 102; DB 3; Length 20;
Best Local Similarity 94.7%; Pred. No. 2e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 24 NPVHFFKNIYVTRTPPPS 42
Db 2 DPVHFFKNIYVTRTPPPS 20

RESULT 28
US-08-468-540B-18
Sequence 18, Application US/08468540B
Patent No. 5858980
GENERAL INFORMATION:
APPLICANT: Weiner, Howard
APPLICANT: Hafner, David
APPLICANT: Miller, Ariel
APPLICANT: Al-Sabbagh, Ahmad
TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby P.C.
STREET: 805 Third Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,540B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jacobs, Seth H
REGISTRATION NUMBER: 32,140
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single

```
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
US-08-468-540B-18

Query Match      38.8%; Score 101; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ENPVVHFKNIVTPRP 40
Db 1 ENPVVHFKNIVTPRP 18

RESULT 29
US-08-468-540B-17
; Sequence 17, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafler, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
US-08-468-540B-17

Query Match      38.5%; Score 100; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFKNIVTPRP 39
Db 1 DENPVVHFKNIVTPRP 18

RESULT 31
US-08-468-540B-19
; Sequence 19, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafler, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
```

; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
; US-08-468-540B-19

Query Match 36.9%; Score 96; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 NPVVHFFKNIVTPRTP 40
Db 1 NPVVHFFKNIVTPRTP 17

RESULT 32
US-09-137-759-3
; Sequence 3, Application US/09137759
; Patent No. 6251396
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Ling, Nicholas C.
; APPLICANT: Staehlin, Theophil
; APPLICANT: Crowe, Paul D.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING
; FILE REFERENCE: 690068.405C1
; CURRENT APPLICATION NUMBER: US/09/137,759
; CURRENT FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis
US-09-137-759-3

Query Match 36.2%; Score 94; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 ENPVVHFFKNIVTPRTP 39
Db 1 ENPVVHFFKNIVTPRTP 17
RESULT 33
US-08-468-540B-20
; Sequence 20, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafner, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
; US-08-468-540B-20

Query Match 35.8%; Score 93; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 DENPVVHFFKNIVTPRTP 38
Db 1 DENPVVHFFKNIVTPRTP 17

RESULT 34
US-08-468-540B-21
; Sequence 21, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafner, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION

```
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
; US-08-468-540B-21

Query Match 33.8%; Score 88; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFKNIVTPR 37
DB 1 DENPVVHFKNIVTPR 16

RESULT 35
US-08-468-540B-10
; Sequence 10, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafler, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
; US-08-468-540B-10

Query Match 33.8%; Score 88; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 KNIVTPRTPPPSQGKG 46
DB 1 KNIVTPRTPPPSQGKG 16

RESULT 36
US-08-297-395-22
; Sequence 22, Application US/08297395A
; Patent No. 6039947
; GENERAL INFORMATION:
; APPLICANT: Howard L. Weiner
; APPLICANT: David A. Hafler
; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
; TITLE OF INVENTION: EPITOPES OF MYELIN BASIC PROTEIN
; FILE REFERENCE: 101/057230S3
; CURRENT APPLICATION NUMBER: US/08/297,395A
; CURRENT FILING DATE: 1994-08-11
; EARLIER APPLICATION NUMBER: 08/059,189
; EARLIER FILING DATE: 1993-05-06
; EARLIER APPLICATION NUMBER: 07/502,559
; EARLIER FILING DATE: 1990-03-30
; EARLIER APPLICATION NUMBER: PCT/US88/02139
; EARLIER FILING DATE: 1988-06-24
; EARLIER APPLICATION NUMBER: 07/065,734
; EARLIER FILING DATE: 1987-06-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-297-395-22

Query Match 33.8%; Score 88; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 KNIVTPRTPPPSQGKG 46
DB 1 KNIVTPRTPPPSQGKG 16

RESULT 37
US-09-153-586-30
```

; Sequence 30, Application US/09153586A
; Patent No. 6270772

; GENERAL INFORMATION:
; APPLICANT: Burrows et al.
; TITLE OF INVENTION: Recombinant MHC molecules useful for manipulation of
; TITLE OF INVENTION: antigen-specific T-Cells
; FILE REFERENCE: 48823

; CURRENT APPLICATION NUMBER: US/09/153,586A

; CURRENT FILING DATE: 1998-09-15

; EARLIER APPLICATION NUMBER: 60/064,552

; EARLIER FILING DATE: 1997-09-16

; EARLIER APPLICATION NUMBER: 60/064,555

; EARLIER FILING DATE: 1997-10-10

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 30

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: artificial

; OTHER INFORMATION: peptide

US-09-153-586-30

Query Match 32.9%; Score 85.5; DB 4; Length 19;
Best Local Similarity 90.0%; Pred. No. 3.1e-05;
Matches 18; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 10 GSLPKSHGRQDENPVVHF 29

DB 1 GSLPKSHGRQDENPVVHF 19

RESULT 38

US-08-468-540B-22

; Sequence 22, Application US/08468540B

; Patent No. 5858980

; GENERAL INFORMATION:

; APPLICANT: Weiner, Howard

; APPLICANT: Hafler, David

; APPLICANT: Miller, Ariel

; APPLICANT: Al-Sabbagh, Ahmad

; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION

; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Darby & Darby P.C.

; STREET: 805 Third Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,540B

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Jacobs, Seth H

; REGISTRATION NUMBER: 32,140

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-527-7700

; TELEFAX:

; TELEX:

; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 5858980e

US-08-468-540B-22

Query Match 31.9%; Score 83; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 5e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFFKNIVTP 36

DB 1 DENPVVHFFKNIVTP 15

RESULT 39

US-08-787-547-37

; Sequence 37, Application US/08787547

; Patent No. 5783567

; GENERAL INFORMATION:

; APPLICANT: Hedley, Mary Lynne

; APPLICANT: Curley, Joanne M.

; APPLICANT: Langer, Robert S.

; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY

; TITLE OF INVENTION: OF NUCLEIC ACID

; NUMBER OF SEQUENCES: 107

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/787,547

; FILING DATE: 22-JAN-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Fraser, Janis K.

; REGISTRATION NUMBER: 34,819

; REFERENCE/DOCKET NUMBER: 08191/003001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-787-547-37

Query Match 31.5%; Score 82; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 6.8e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ENPVVHFFKNIVTP 37

DB 1 ENPVVHFFKNIVTP 15

```

: CITY: BOSTON
: STATE: MA
: COUNTRY: USA
: ZIP: 02210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/400,796
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: TWOMEY, MICHAEL J.
: REGISTRATION NUMBER: 38,349
: REFERENCE/DOCKET NUMBER: H0498/7015
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-720-3500
: TELEFAX: 617-720-2441
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: FRAGMENT TYPE: Internal
: ORIGINAL SOURCE:
: ORGANISM: HOMO SAPIENS
: US-08-400-796-16

Query Match 31.5%; Score 82; DB 2; Len
Best Local Similarity 100.0%; Pred. No. 6.8e-05;
Matches 15; Conservative 0; Mismatches 0;

QY 23 ENPVVHEFKNIVTPR 37
DB 1 ENPVVHEFKNIVTPR 15
|||||||
|||||||

RESULT 42
US-09-153-586-25
: Sequence 25, Application US/09153586A
: Patent No. 6270772
: GENERAL INFORMATION:
: APPLICANT: Burrows et al.
: TITLE OF INVENTION: Recombinant MHC molecules useful
: TITLE OF INVENTION: antigen-specific T-Cells
: FILE REFERENCE: 48823
: CURRENT APPLICATION NUMBER: US/09/153,586A
: EARLIER FILING DATE: 1998-09-15
: EARLIER APPLICATION NUMBER: 60/064,552
: EARLIER FILING DATE: 1997-09-16
: EARLIER APPLICATION NUMBER: 60/064,555
: EARLIER FILING DATE: 1997-10-10
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 25
: LENGTH: 19
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence
: OTHER INFORMATION: peptide
US-09-153-586-25

Query Match 31.3%; Score 81.5; DB 4; Len
Best Local Similarity 85.0%; Pred. No. 0.0001;
Matches 17; Conservative 1; Mismatches 1;

```

QY 10 GSLPQKSHGRTQDENPVVHF 29
Db 1 GSLPQKSG-RSQDENPVVHF 19

RESULT 43

US-08-468-540B-23
; Sequence 23, Application US/08468540B
; Patent No. 5858980
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Hafner, David
; APPLICANT: Miller, Ariel
; APPLICANT: Al-Sabbagh, Ahmad
; TITLE OF INVENTION: SUPPRESSION OF T-CELL PROLIFERATION
; TITLE OF INVENTION: USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,540B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jacobs, Seth H
; REGISTRATION NUMBER: 32,140
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5858980e
US-08-468-540B-23

Query Match 29.6%; Score 77; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 NPVHFFKNIVTPR 37
Db 1 NPVHFFKNIVTPR 14

RESULT 44

US-08-787-547-36
; Sequence 36, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langet, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID

; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-36

Query Match 29.2%; Score 76; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DENPVVHFFKNIVT 35
Db 1 DENPVVHFFKNIVT 14

RESULT 45

US-08-342-408B-3
; Sequence 3, Application US/08342408B
; Patent No. 6329499
; GENERAL INFORMATION:
; APPLICANT: Ling, Nicholas
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; APPLICANT: Steinman, Lawrence
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE
; TITLE OF INVENTION: SCLEROSIS USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,408B

```
;
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 632949tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 690068.405
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-342-408B-3

Query Match      29.2%; Score 76; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. NO. 0.0004;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 VVHFFKNIVTPTP 39
Db 1 VVHFFKNIVTPTP 14
```

Search completed: September 23, 2002, 11:09:18
Job time: 22 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 23, 2002, 11:08:56 ; Search time 18.03 Seconds
(without alignments)
245.153 Million cell updates/sec

Title: US-09-813-383-1

Perfect score: 260

Sequence: 1 HHPARTAHYGLFQKSHGRT.....VHFFKNIVTPRTPPSQGK 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 5486

Minimum DB seq length: 0

Maximum DB seq length: 27

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	77	29.6	14	2	SL2904
2	39	15.0	26	2	B49413
3	35	13.5	23	2	C56978
4	34	13.1	22	2	I41299
5	34	13.1	25	2	I40692
6	31	11.9	15	2	I67525
7	31	11.9	18	2	S27141
8	31	11.9	20	2	A31516
9	31	11.9	21	2	B29663
10	30	11.5	16	2	JH0517
11	30	11.5	21	2	PC7043
12	30	11.5	26	2	D27262
13	29	11.2	13	2	G37266
14	29	11.2	13	2	B61457
15	29	11.2	18	2	B24735
16	29	11.2	21	2	S29858
17	29	11.2	23	2	A29551
18	29	11.2	25	2	B49111
19	29	11.2	26	2	A24735
20	29	11.2	26	2	I49748
21	28	10.8	17	2	I67526
22	28	10.8	18	2	S46241
23	28	10.8	20	2	A33878
24	28	10.8	22	2	S07394
25	28	10.8	23	2	S45030
26	28	10.8	26	2	PH1704
27	27	10.4	11	2	PT0287
28	27	10.4	14	2	SL1129
29	27	10.4	18	2	H64711

30 27 10.4 18 2 A54195 Na+/K+-exchanging
31 27 10.4 20 2 D49164 chromogranin-B - r
32 27 10.4 24 2 T42258 Ser/Thr protein ph
33 27 10.4 25 2 PH1701 Ig heavy chain V r
34 27 10.4 25 2 B32351 39K class A flagel
35 27 10.4 26 2 C41499 alpha-antigen C, e
36 27 10.4 27 2 A44629 homeotic protein H
37 26.5 10.2 27 1 SRAPC protamine B - Russ
38 26 10.0 7 2 S71299 ICL2 protein - Par
39 26 10.0 10 2 A36454 trypsin-modulating
40 26 10.0 11 2 A14454 6-phosphofructokin
41 26 10.0 13 2 D39690 neural cell adhesi
42 26 10.0 15 2 PT0037 light harvesting c
43 26 10.0 16 2 JN0264 translation initia
44 26 10.0 17 2 S59481 hydroxyproline-ric
45 26 10.0 17 2 D48138 d(TTAGG)n-binding

ALIGNMENTS

RESULT 1

SL2904

protein kinase (EC 2.7.1.37) - starfish (Pisaster ochraceus)

C:Species: Pisaster ochraceus

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997

C:Accession: SL2904

R:Sanghera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.

FEBS Lett. 273, 223-226, 1990

A:Title: Identification of the sites in myelin basic protein that are phosphorylated

A:Reference number: SL2904; MUID:91032186

A:Accession: SL2904

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <S>

C:Keywords: phosphotransferase

Query Match 29.6%; Score 77; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 NIVTPRTPPPSQGK 45

Db 1 NIVTPRTPPPSQGK 14

RESULT 2

B49413

perilipin B - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995

C:Accession: B49413

R:Greenberg, A.S.; Egan, J.J.; Wek, S.A.; Moos Jr., M.C.; Londres, C.; Kimmel, A.R.

Proc. Natl. Acad. Sci. U.S.A. 90, 12035-12039, 1993

A:Title: Isolation of cDNAs for perilipins A and B: sequence and expression of lipid

A:Reference number: A49413; MUID:94089764

A:Accession: B49413

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-26 <G>

A:Experimental source: adipocytes

A>Note: sequence extracted from NCBI backbone (NCBIN:141052, NCBI:141054)

Query Match 15.0%; Score 39; DB 2; Length 26;

Best Local Similarity 42.9%; Pred. No. 1.8e+02;

Matches 9; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 26 VHHFFKNIVTPRTPPPSQGK 46

Db 5 VHHYVP--VSPAPGPPSDSG 23

RESULT 3

C56978

collagen alpha 1(II) chain - bovine (fragment)
 N:Alternate names: collagen alpha 3(XI) chain
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 05-Dec-1998
 C:Accession: C56978

R:Wu, J.J.; Eyre, D.R.

J. Biol. Chem. 270, 18865-18870, 1995

A:Title: Structural analysis of cross-linking domains in cartilage type XI collagen. In:
 A:Reference number: A56978; MUID:95370194

A:Accession: C56978

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-23 <WDA>

C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

C:Keywords: hydroxylysine; hydroxyproline

F:5/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental

F:8/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match

Best Local Similarity 13.5%; Score 35; DB 2; Length 23;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY

33 IVTPPTPPPSQG 44

||| | | | | |

Db 1 IVGPKGPPQSG 12

RESULT 4

I41299

T-cell receptor beta chain precursor V region (6.10) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 23-Jul-1999

C:Accession: I41299

R:Uematsu, Y.; Wege, H.; Straus, A.; Ott, M.; Bannwarth, W.; Lanchbury, J.; Panayi, G.;

Proc. Natl. Acad. Sci. U.S.A. 88, 8534-8538, 1991

A:Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheumatoid
 A:Reference number: A41299; MUID:92020887

A:Accession: I41299

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-22 <UEM>

A:Cross-references: GB:S57506; NID:q236334; PIDN:AAB19964.1; PID:q236335

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 13.1%; Score 34; DB 2; Length 22;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY

19 RTQDENPVVH 28

||| | | | | |

Db 8 RTQEDPAVH 17

RESULT 5

I40692

cena protein (IgAlh) - Cellulomonas fimi (fragment)

C:Species: Cellulomonas fimi

C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 22-Oct-1999

C:Accession: I40692

R:Miller, P.B.; Shen, H.; Gilkes, N.R.; Kilburn, D.G.; Miller, R.C.; Plaut, A.G.; Warren

FEMS Microbiol. Lett. 92, 199-204, 1992

A:Title: Endoglucanase A from Cellulomonas fimi in which the hinge sequence of human IgA
 hoese.

A:Reference number: I40692

A:Accession: I40692

A>Status: preliminary; translated from GB/EMBL/DDBT

A:Molecule type: DNA

A:Residues: 1-25 <RES>

A:Cross-references: EMBL:X65780; NID:g312035; PIDN:CAA46663.1; PID:g312036

Query Match

Best Local Similarity 13.1%; Score 34; DB 2; Length 25;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY

32 NIVTPPTPPPS 42

:: ||| | | | |

Db 2 SVSTPTTTPSPS 12

RESULT 6

I67525

CD33 antigen homolog - mouse (fragment)

C:Species: Mus sp. (mouse)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Jun-1998

C:Accession: I67525

R:Chies, J.A.; Lembezat, M.P.; Freitas, A.A.

Eur. J. Immunol. 24, 1657-1664, 1994

A:Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice i

A:Reference number: I53392; MUID:94298870

A:Accession: I67525

A>Status: preliminary; translated from GB/EMBL/DDBT

A:Molecule type: mRNA

A:Residues: 1-15 <RES>

A:Cross-references: GB:S71349; NID:g550037

C:Genetics:

A:Gene: Ig VH7183

Query Match

Best Local Similarity 11.9%; Score 31; DB 2; Length 15;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

4 ARTAHYGS 11

||| | | | |

Db 3 ARRDHYGS 10

RESULT 7

S27141

hypothetical protein 2 estrogen receptor 5'-region - human

C:Species: Homo sapiens (man)

C>Date: 05-May-1994 #sequence_revision 12-May-1995 #text_change 18-Aug-2000

C:Accession: S27141

R:Keaveney, M.; Klug, J.; Gannon, F.

DNA Seq. 2, 347-358, 1992

A:Title: Sequence analysis of the 5' flanking region of the human estrogen receptor g

A:Reference number: S27140; MUID:93075998

A:Accession: S27141

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-18 <KEA>

A:Cross-references: EMBL:X62462; NID:g31201; PIDN:CAA44320.1; PID:g31203

C:Genetics:

A:Introns: 13/2

C:Superfamily: unassigned leader peptides

Query Match

Best Local Similarity 11.9%; Score 31; DB 2; Length 18;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY

28 HFFKNTVTP 36

||| | | | |

Db 3 HEWKDVLDP 11

RESULT 8

A31516

lectin, galactose/N-acetylgalactosamine-specific - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)
 C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
 C;Accession: A31516
 R;II, M.; Kawasaki, T.; Yamashina, I.
 Biochem. Biophys. Res. Commun. 155, 720-725, 1988
 A;Title: Structural similarity between the macrophage lectin specific for galactose/N-acetylglucosamine
 A;Reference number: A31516; MUID:88339956
 A;Accession: A31516
 A;Molecule type: protein
 A;Residues: 1-20 <II>

Query Match 11.9%; Score 31; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 31 KNIVPTPTPPPS 42
 II : IIII
 Db 8 KNDEAGKAPPPS 19

RESULT 9
 B29663
 histone H2B - starfish (Pisaster ochraceus) (fragments)
 C;Species: Pisaster ochraceus
 C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
 C;Accession: B29663
 R;Howell, A.M.; Cool, D.; Hewitt, J.; Ydenberg, B.; Smith, M.J.; Honda, B.M.
 J. Mol. Evol. 25, 29-36, 1987
 A;Title: Organization and unusual expression of histone genes in the sea star Pisaster
 A;Reference number: A92968
 A;Accession: B29663
 A;Molecule type: DNA
 A;Residues: 1-21 <HOW>

Query Match 11.9%; Score 31; DB 2; Length 21;
 Best Local Similarity 62.5%; Pred. No. 1.4e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 39 PPPSQGK 45
 II : IIII
 Db 2 PPKASGK 9

RESULT 10
 JH0517
 insulin-like growth factor-binding protein 4 - pig (fragment)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 23-Mar-1995
 C;Accession: JH0517
 R;Coleman, M.E.; Pan, Y.C.E.; Etherton, T.D.
 Biochem. Biophys. Res. Commun. 181, 1131-1136, 1991
 A;Title: Identification and NH2-terminal amino acid sequence of three insulin-like growth
 A;Reference number: JH0515; MUID:92109718
 A;Accession: JH0517
 A;Molecule type: protein
 A;Residues: 1-16 <COL>
 A;Experimental source: serum

Query Match 11.5%; Score 30; DB 2; Length 16;
 Best Local Similarity 71.4%; Pred. No. 1.3e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 39 PPPSQK 45
 IIII : I
 Db 7 PPPSEK 13

RESULT 11
 PC7043
 ubiquitin carboxyl-terminal hydrolase (EC 3.1.1.-) homolog - yeast (Pichia anomala) (fra

N;Alternate names: ALX1 protein
 C;Species: Pichia anomala, Candida pelliculosa
 C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
 C;Accession: PC7043
 R;Sakajo, S.; Minagawa, N.; Yoshimoto, A.
 Biosci. Biotechnol. Biochem. 63, 1889-1894, 1999
 A;Title: Structure and regulatory expression of a single copy alternative oxidase gene
 A;Reference number: JC7145; MUID:20101471
 A;Accession: PC7043
 A;Molecule type: DNA
 A;Residues: 1-21 <SAK>
 A;Cross-References: DDBJ:AB026726
 C;Genetics: alx1
 C;Keywords: hydrolase

Query Match 11.5%; Score 30; DB 2; Length 21;
 Best Local Similarity 31.6%; Pred. No. 1.8e+03;
 Matches 6; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 4 ARTAHYGLPKSGHRTQD 22
 I : II :
 Db 3 AKEAKVGSVEDKREGEKEE 21

RESULT 12
 D27262
 nicotinic acetylcholine receptor delta chain - electric eel (fragment)
 C;Species: Electrophorus electricus (electric eel)
 C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 15-Jun-1996
 C;Accession: D27262
 R;Conti-Ironconi, B.M.; Hunkapiller, M.W.; Lindstrom, J.M.; Raftery, M.A.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6489-6493, 1982
 A;Title: Subunit structure of the acetylcholine receptor from Electrophorus electricus
 A;Reference number: A93932; MUID:83065199
 A;Accession: D27262
 A;Molecule type: protein
 A;Residues: 1-26 <CON>
 C;Superfamily: acetylcholine receptor
 C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra

Query Match 11.5%; Score 30; DB 2; Length 26;
 Best Local Similarity 38.5%; Pred. No. 2.3e+03;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 19 RTQDENPVVRFK 31
 I : II : III
 Db 1 RNEERLINHLFK 13

RESULT 13
 G37266
 Ig heavy chain C region (PV2) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
 C;Accession: G37266
 R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
 J. Biol. Chem. 266, 6607-6613, 1991
 A;Title: Heavy and light chain variable region sequences and antibody properties of a
 A;Reference number: A38740; MUID:91177923
 A;Accession: G37266
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-13 <RUF>

Query Match 11.2%; Score 29; DB 2; Length 13;
 Best Local Similarity 71.4%; Pred. No. 1.4e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 37 RTPPPSQ 43

C:Accession: A24735
 R:Mannervik, B.; Alin, P.; Guthenberg, C.; Jansson, H.; Tahir, M.K.; Warholm, M.; Jorhva
 Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985
 A:Title: Identification of three classes of cytosolic glutathione transferase common to
 A:Reference number: A24735; MUID:86042634

A:Accession: A24735
 A:Molecule type: protein
 A:Residues: 1-26 <MAN>
 C:Superfamily: glutathione transferase
 C:Keywords: transferase

Query Match 11.2%; Score 29; DB 2; Length 26;
 Best Local Similarity 66.7%; Pred. No. 3.1e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 25 PVVHFF 30
 |||:|
 Db 5 PVLHYF 10

RESULT 20

149748
 homeobox protein - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 15-Oct-1999
 C:Accession: I49748
 R:Dear, T.N.; Sanchez-Garcia, I.; Rabbitts, T.H.
 Proc. Natl. Acad. Sci. U.S.A. 90, 4431-4435, 1993
 A:Title: The HOX11 gene encodes a DNA-binding nuclear transcription factor belonging to
 A:Reference number: A47433; MUID:93281593

A:Accession: I49748
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-26 <RES>

A:Cross-references: GB:L08617; NID:g309311; PIDN:AAA37829.1; PID:g309312
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 11.2%; Score 29; DB 2; Length 26;
 Best Local Similarity 50.0%; Pred. No. 3.1e+03;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 6 TAHYGLPKSH 17
 |||:|
 Db 1 TQYLSPPKKH 12

RESULT 21

167526
 CD33 antigen homolog - mouse (fragment)
 C:Species: Mus sp. (mouse)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Jun-1998
 C:Accession: I67526
 R:Chies, J.A.; Lembezat, M.P.; Freitas, A.A.
 Eur. J. Immunol. 24, 1657-1664, 1994
 A:Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is r

A:Reference number: I53392; MUID:94298870
 A:Accession: I67526
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-17 <RES>
 A:Cross-references: GB:S71350; NID:g550038
 C:Genetics:
 A:Gene: VH7183

Query Match 10.8%; Score 28; DB 2; Length 17;
 Best Local Similarity 62.5%; Pred. No. 2.5e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ARTAHYGS 11

|||:|
 Db 3 ARRAYGN 10

RESULT 22

S46241
 NAD(P)H-flavin oxidoreductase (EC 1.-.-.-) - Vibrio fischeri
 C:Species: Vibrio fischeri
 C:Date: 10-Dec-1994 #sequence_revision 12-May-1995 #text_change 16-Oct-1998
 C:Accession: S46241
 R:Inouye, S.

FEBS Lett. 347, 163-168, 1994
 A:Title: NAD(P)H-flavin oxidoreductase from the bioluminescent bacterium, Vibrio fisc
 A:Reference number: S46241; MUID:94307374
 A:Accession: S46241

A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-18 <INO>
 C:Keywords: NAD; oxidoreductase

Query Match 10.8%; Score 28; DB 2; Length 18;
 Best Local Similarity 28.6%; Pred. No. 2.7e+03;
 Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 24 NPVHFFKNIIVTPR 37
 |||:|
 Db 2 HPIIHDLNRYTSK 15

RESULT 23

A33878
 myosin light chain kinase, smooth muscle - turkey (fragment)
 C:Species: Meleagris gallopavo (common turkey)
 C:Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 07-Nov-1997
 C:Accession: A33878

R:Ikebe, M.; Maruta, S.; Reardon, S.
 J. Biol. Chem. 264, 6967-6971, 1989
 A:Title: Location of the inhibitory region of smooth muscle myosin light chain kinase
 A:Reference number: A33878; MUID:89214114
 A:Accession: A33878

A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <IKB>
 C:Superfamily: myosin-light-chain kinase, nonmuscle; fibronectin type III repeat homo
 C:Keywords: smooth muscle

Query Match 10.8%; Score 28; DB 2; Length 20;
 Best Local Similarity 80.0%; Pred. No. 3e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 36 PRTTP 40
 |||
 Db 5 PRTTP 9

RESULT 24

S07394
 DNA-invertase - phage D108 (fragment)
 C:Species: phage D108

A:Note: host Escherichia coli
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C:Accession: S07394
 R:Sztamari, G.B.; Lapointe, M.; DuBow, M.S.
 Nucleic Acids Res. 15, 6691-6704, 1987

A:Title: The right end of transposable bacteriophage D108 contains a 520 base pair pr
 A:Reference number: S07394; MUID:87316928

A:Accession: S07394
 A:Molecule type: DNA
 A:Residues: 1-22 <SZ>

A:Cross-references: EMBL:X05926; NID:g14918; PIDN:CAA29365.1; PID:g1364174
 C:Genetics:

A:Gene: gin
 C:Superfamily: transposase repressor
 C:Keywords: DNA binding; DNA integration; DNA recombination

Query Match 10.8%; Score 28; DB 2; Length 22;
 Best Local Similarity 57.1%; Pred. No. 3.4e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HPARTAH 8
 |||: |
 Db 4 HPAKRTH 10

RESULT 25
 S45030
 homeotic protein SPOX H1 - Haliclona sp. (fragment)
 C:Species: Haliclona sp.
 C:Date: 06-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 15-Oct-1999
 C:Accession: S45030
 R:Degnan, B.M.; Degnan, S.M.; Giusti, A.; Morse, D.E.
 submitted to the EMBL Data Library, May 1994
 A:Description: A Hox homeobox gene in sponges.
 A:Reference number: S45030
 A:Accession: S45030
 A:Molecule type: DNA
 A:Residues: 1-23 <DEG>
 A:Cross-references: EMBL:X79263; NID:g488754; PIDN:CA455850.1; PID:g488755
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 10.8%; Score 28; DB 2; Length 23;
 Best Local Similarity 30.4%; Pred. No. 3.5e+03;
 Matches 7; Conservative 3; Mismatches 5; Indels 8; Gaps 1;

QY 9 YGSLPOKSHGRQDENPVVHFFK 31
 |||:||||:|
 Db 4 YLSLTERSH-----IAHLK 18

RESULT 26
 PH1704
 Ig heavy chain V region (clone NP-7-17) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
 C:Accession: PH1704
 R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
 J. Exp. Med. 178, 295-307, 1993
 A:Title: Antigen-driven B cell differentiation in vivo.
 A:Reference number: PH1675; MUID:93301607
 A:Accession: PH1704
 A:Molecule type: mRNA
 A:Residues: 1-26 <MCH>
 A:Experimental source: B cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 10.8%; Score 28; DB 2; Length 26;
 Best Local Similarity 62.5%; Pred. No. 4.1e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 ARTAHYGS 11
 ||:||||
 Db 13 ARISYYS 20

RESULT 27
 PT0287
 Ig heavy chain CRD3 region (clone 4-103) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0287
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
 A:Reference number: PT0222; MUID:91108337
 A:Accession: PT0287
 A:Molecule type: DNA
 A:Residues: 1-11 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 10.4%; Score 27; DB 2; Length 11;
 Best Local Similarity 44.4%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 HHPARTAHY 9
 | |||:
 Db 2 HEAGRTQHF 10

RESULT 28
 S1129
 phosphoprotein, bone - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 25-Oct-1996
 C:Accession: S1129
 R:Mikuni-Takagaki, Y.; Glimcher, M.J.
 Biochem. J. 268, 585-591, 1990
 A:Title: Post-translational processing of chicken bone phosphoproteins. Identification
 A:Reference number: S1127; MUID:90303246
 A:Accession: S1129
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <MIK>
 C:Keywords: phosphoprotein

Query Match 10.4%; Score 27; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 2.7e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 36 PRTPPP 41
 | |||
 Db 2 PAAPPP 7

RESULT 29
 H64711
 hypothetical protein HP1536 - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
 C:Accession: H64711
 R:Tom, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Pleischmann, R.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467
 A:Accession: H64711
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-18 <TOM>
 A:Cross-references: GB:AE000651; GB:AE000511; NID:g2314708; PIDN:AA008578.1; PID:g231

Query Match 10.4%; Score 27; DB 2; Length 18;
 Best Local Similarity 44.4%; Pred. No. 3.6e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HHPARTAHY 9
 :|||:|

Db 9 NHPSRNPKY 17

RESULT 30

A54195
Nat/K+-exchanging ATPase (EC 3.6.1.37) - spiny dogfish (fragment)
C:Species: Squalus acanthias (spiny dogfish)
C:Date: 13-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: A54195
R:Esmann, M.; Karlisch, S.J.; Sottrup-Jensen, L.; Marsh, D.
Biochemistry 33, 8044-8050, 1994
A:Title: Structural integrity of the membrane domains in extensively trypsinized Na,K-ATPase
A:Reference number: A54195; MUID: 94297020
A:Accession: A54195
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <ES>
A:Experimental source: rectal gland
A:Note: sequence extracted from NCBI backbone (NCBIP:149363)
C:Keywords: hydrolase

Query Match 10.4%; Score 27; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 38 TTPPS 42
|||:
Db 7 TPPT 11

RESULT 31

D49164
Chromogranin-B - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-May-1997
C:Accession: D49164
R:Nielsen, E.; Wellinder, B.S.; Madsen, O.D.
Endocrinology 129, 3147-3156, 1991
A:Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides th
A:Reference number: A49164; MUID: 92063871
A:Accession: D49164
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <NIE>
A:Note: sequence extracted from NCBI backbone (NCBIP:66368)
C:Superfamily: chromogranin B precursor

Query Match 10.4%; Score 27; DB 2; Length 20;
Best Local Similarity 32.0%; Pred. No. 4e+03;
Matches 8; Conservative 1; Mismatches 4; Indels 12; Gaps 2;

Qy 1 HHPARTAHYGLPKSHGRTQDENP 25
|||
Db 2 HH---LAHY-----RASEEP 14

RESULT 32

T42258
Ser/Thr protein phosphatase homolog - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C:Accession: T42258
R:Zeke, T.; Gergely, P.; Dombradi, V.
submitted to the EMBL Data Library, July 1996
A:Description: The catalytic subunits of Ser/Thr protein phosphatases from Caenorhabdit
A:Reference number: Z22131
A:Accession: T42258
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-24 <ZEK>
A:Cross-references: EMBL:Z77734; PIDN:CAE01293.1

C:Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprot

Query Match 10.4%; Score 27; DB 2; Length 24;
Best Local Similarity 28.6%; Pred. No. 4.9e+03;
Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 27 VHFKNIVTPRTPP 40
:| : :| :|
Db 3 IHLRLILMTCDAPP 16

RESULT 33

PH1701
Ig heavy chain V region (clone NP-7-14) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1701
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID: 93301607
A:Accession: PH1701
A:Molecule type: mRNA
A:Residues: 1-25 <MCH>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 10.4%; Score 27; DB 2; Length 25;
Best Local Similarity 62.5%; Pred. No. 5.1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ARTAHYGS 11
|| : :| :|
Db 13 ARYSYGS 20

RESULT 34

B32351
39K class A flagellar protein, periplasmic - Treponema phagedenis (fragment)
C:Species: Treponema phagedenis
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 26-May-2000
C:Accession: B32351
R:Norris, S.J.; Charon, N.W.; Cook, R.G.; Fuentes, M.D.; Limberger, R.J.
J. Bacteriol. 170, 4072-4082, 1988
A:Title: Antigenic relatedness and N-terminal sequence homology define two classes of
A:Reference number: A91882; MUID: 88314903
A:Accession: B32351
A:Molecule type: protein
A:Residues: 1-25 <NOR>
C:Superfamily: spirochete flagellar sheath protein

Query Match 10.4%; Score 27; DB 2; Length 25;
Best Local Similarity 50.0%; Pred. No. 5.1e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 12 LPQKSHGRTQ 21
:| : :| :|
Db 16 VPDKNGGMTQ 25

RESULT 35

C41499
alpha-antigen C, extracellular - Mycobacterium bovis (fragment)
N:Alternate names: antigen 85A; antigen P32
C:Species: Mycobacterium bovis
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 09-Jun-2000
C:Accession: C41499; A61471
R:Wiker, H.G.; Sletten, K.; Nagai, S.; Harboe, M.
Infect. Immun. 58, 272-274, 1990

A:Title: Evidence for three separate genes encoding the proteins of the mycobacterial an
 A:Reference number: A41499; MUID:90093478
 A:Accession: C41499
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-26 <WIK>
 R:De Bruyn, J.; Huygen, K.; Bosmans, R.; Fauville, M.; Lippens, R.; Van Vooren, J.P.; Fa
 Microb. Pathog. 2, 351-366, 1987
 A:Title: Purification, characterization and identification of a 32 kDa protein antigen o
 A:Reference number: A61471; MUID:89180951
 A:Accession: A61471
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-6 <DEA>
 C:Superfamily: Mycobacterium avium alpha-antigen

Query Match 10.4%; Score 27; DB 2; Length 26;
 Best Local Similarity 35.3%; Pred. No. 5.4e+03;
 Matches 6; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 PARTAHYGLPKSHGR 19
 | | | | |
 DB 4 PGLFVEYLQVPSASMG 20

RESULT 36
 A44629
 homeotic protein Hox 2 (clone 2d) - Florida lancelet (fragment)
 C:Species: Branchiostoma floridae (Florida lancelet)
 C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 15-Oct-1999
 C:Accession: A44629
 R:Pendleton, J.W.; Nagai, B.K.; Murtha, M.T.; Ruddle, F.H.
 Proc. Natl. Acad. Sci. U.S.A. 90, 6300-6304, 1993
 A:Title: Expansion of the Hox gene family and the evolution of chordates.
 A:Reference number: A44616; MUID:93317669
 A:Accession: A44629
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-27 <PEN>
 A:Cross-references: GB:L14878; NID:g289459; PID:AAA02514.1; PID:g289460
 C:Superfamily: unassigned homeobox proteins; homeobox homology
 C:Keywords: DNA binding; embryo; homeobox; nucleus; transcription regulation

Query Match 10.4%; Score 27; DB 2; Length 27;
 Best Local Similarity 50.0%; Pred. No. 5.6e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 28 HFFKNIVTPR 37
 | | | | |
 DB 1 HFNKYVCKPR 10

RESULT 37
 SRAPC
 protamine B - Russian sturgeon
 R:Alternate names: sturine
 C:Species: Acipenser gueldenstaedti (Russian sturgeon)
 C:Date: 12-Aug-1981 #sequence_revision 12-Aug-1981 #text_change 16-Feb-1997
 C:Accession: A02665
 R:Yulikova, E.P.; Evseenko, L.K.; Baratova, L.A.; Belyanova, L.P.; Rybin, V.K.; Silaev,
 Bioorg. Khim. 2, 1613-1617, 1976
 A:Reference number: A02665
 A:Accession: A02665
 A:Molecule type: protein
 A:Residues: 1-27 <YUL>
 C:Superfamily: protamine Y2
 C:Keywords: chromosomal protein; DNA binding; spermatogenesis

Query Match 10.2%; Score 26.5; DB 1; Length 27;

Best Local Similarity 38.1%; Pred. No. 6.5e+03;
 Matches 8; Conservative 1; Mismatches 7; Indels 5; Gaps 1;

QY 4 ARTAHYGLPQ-----KSHGR 19
 | | | | | : | | |
 DB 1 ARRRRSSRPORRRRRHGR 21

RESULT 38
 ICL2 protein - Paramacium tetraurelia (fragment)
 C:Species: Paramacium tetraurelia
 C:Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-Dec-1999
 C:Accession: S71299
 R:Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.
 Eur. J. Biochem. 238, 121-128, 1996
 A:Title: Characterization of centrin genes in Paramacium.
 A:Reference number: S71298; MUID:96248429
 A:Accession: S71299
 A:Molecule type: protein
 A:Residues: 1-7 <MAD>
 A:Experimental source: strain d4-2
 C:Genetics:
 A:Genetic code: SGC5

Query Match 10.0%; Score 26; DB 2; Length 7;
 Best Local Similarity 80.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 PPPPQ 43
 | | | |
 DB 3 PPPQQ 7

RESULT 39
 A36454
 trypsin-modulating oostatic factor - yellow fever mosquito
 C:Species: Aedes aegypti (yellow fever mosquito)
 C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-May-1996
 C:Accession: A36454; A61630
 R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
 FASB J. 4, 3015-3020, 1990
 A:Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme
 A:Reference number: A36454; MUID:90367888
 A:Accession: A36454
 A:Molecule type: protein
 A:Residues: 1-10 <BOR>
 R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
 Insect Biochem. Mol. Biol. 23, 703-712, 1993
 A:Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating o
 A:Reference number: A61630; MUID:93357794
 A:Accession: A61630
 A:Molecule type: protein
 A:Residues: 1-10 <BO2>
 A:Note: none of the amino acids is modified
 C:Function:
 A:Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut
 C:Keywords: hormone

Query Match 10.0%; Score 26; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 36 PRTPPP 41
 | | | |
 DB 3 PAPPPP 8

RESULT 40
 A14454
 6-phosphofructokinase (EC 2.7.1.11) - sheep (fragment)

C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Date: 05-Jun-1987 sequence_revision 05-Jun-1987 text_change 28-Apr-1993
C.Accession: AL4454
R.Fordyce, A.M.: Midwinter, G.G.; Moore, C.H.
Biochem. Soc. Trans. 7, 721-723, 1979
A.Title: the N-terminal amino acid sequence of sheep heart phosphofructokinase.
A.Reference number: AL4454; MUID:80004524
A.Accession: AL4454
A.Molecule type: protein
A.Residues: 1-11 <FOR>
C.Keywords: glycolysis; phosphotransferase

```
Query Match      10.0%; Score 26; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

Qy	1	HHPART	6
D6	5	HHEAKT	10

RESULT 41

D39690
neural cell adhesion molecule, cardiac splice form +, -, + - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Jul-1999
C:Accession: D39690
R:Reyes, A.A.; Small, S.J.; Akeson, R.
Mol. Cell. Biol. 11, 1654-1661, 1991
A:Title: At least 27 alternatively spliced forms of the neural cell adhesion molecule mRNA
A:Reference number: A39690; MUID:91l141516
A:Accession: D39690
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-13 <REY>
A:Cross-references: GB:M63970
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like
C:Keywords: cardiac muscle; cell adhesion; heart

```
Query Match      10.0%; Score 26; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

QY 36 PRTPPSQGK 45
| | | | |
Db 2 PVHSPPPQGF 11

RESULT

PT0037
light harvesting complex chain III/b, photosystem I - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C:Accession: PT0037; PS0205
R:Uchiyama, Y.; Tsugita, A.
submitted to JIPID, June 1991
A:Reference number: PS0189
A:Accession: PT0037
A:Molecule type: protein
A:Residues: 1-15 <UCH>

```
Query Match      10.0%; Score 26; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 3.8e+03;
Matches      4: Conservative      1: Mismatches      2: Indels      0: Gaps      0:
```

Qy	36	PRTPPPS	42
		III:	
Db	9	PPPPPPA	15

```

RESULT 43
JN0264
translation initiation factor eIF-2 gamma chain - pig (fragment)
N:Alternate names: eIF2 gamma chain
N:Alternative: Sus scrofa domestica (domestic pig)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 0
C:Accession: JN0264
R:Mukoyama, E.B.; Shiokawa, H.; Suzuki, H.
Biosci. Biotechnol. Biochem. 56, 680-681, 1992
A:Title: GTP-binding sequences in the gamma subunit of pig liver
A:Reference number: JN0264; MUID:92282179
A:Accession: JN0264
A:Molecule type: protein
A:Residues: 1-16 <MOK>
A:Experimental source: liver
C:Keywords: GTP binding
F:1-16/Region: GTP binding #status experimental

```

Query Match	10.0%	Score 26;	DB 2;	Length 16;
Best Local Similarity	28.6%	Pred. No. 4.le+03;		
Matches	4:	Conservative	5:	Mismatches 5; Indels 0; Gaps 0;

Qy 6 TAHYGSLPQKSHGR 19
| : | : | :
Db 3 TINIGTIGHVAHGK 16

RESULT 44

S59481
hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)
C:Species: Phaseolus vulgaris (kidney bean)
C:Date: 27-Apr-1996 #sequence_revision 19-Jul-1996 #text_change 05-Dec-1998
C:Accession: S59481
R:Wojtaszek, P.; Trethowan, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A:Title: Specificity in the immobilisation of cell wall proteins in response to differ
A:Reference number: S59481, MUID: 96011753
A:Accession: S59481
A:Molecule type: protein
A:Residues: 1-17 <WOU>
C:Keywords: glycoprotein; hydroxyproline
F:6.8.9.10.11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 10.0%; Score 26; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 4.4e+03;
Matches 4: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	36	PRTPPP	41
nb	5	ppvppp	10

RESULT 45

d(TRAGG)n-binding protein B37 - human (fragment)
 N:Alternate names: type A-B heterogeneous nuclear ribonucleoprotein homolog
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
 C:Accession: D48138
 R:Ishikawa, F.; Matunis, M.J.; Dreyfuss, G.; Cech, T.R.
 Mol. Cell. Biol. 13, 4301-4310, 1993
 A:Title: Nuclear proteins that bind the pre-mRNA 3' splice site sequence r(U
 A:Reference number: A48138; MUID:93309464
 A:Accession: D48138
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-17 <1SH>
 A:Experimental source: HeLa cell nuclei
 A:Note: sequence extracted from NCBI backbone (NCBI:P:134642)

Query Match 10.0%; Score 26; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 4.4e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 38 TPPPSQK 45
|||:
Db 10 TPDPNTGR 17

Search completed: September 23, 2002, 11:09:43
Job time: 47 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 23, 2002, 11:08:57 ; Search time 10.15 Seconds
(without alignments)
175.478 Million cell updates/sec

Title: US-09-813-383-1

Perfect score: 260

Sequence: 1 HHPARTAHYGLSLPKSHGRT.....VHFFKNIVTPRTPPSQGKG 46

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 1612

Minimum DB seq length: 0

Maximum DB seq length: 27

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	30	11.5	16	1	IBP4_PIG
2	30	11.5	26	1	ACHD_ELEEL
3	28	10.8	14	1	RS19_PPWPB
4	28	10.8	22	1	DNIV_BPD10
5	28	10.8	25	1	AMP3_MELGA
6	27	10.4	19	1	DURC_STRGP
7	27	10.4	20	1	YQAH_KLEAE
8	27	10.4	25	1	FLAA_TREPH
9	26.5	10.2	27	1	PRIB_ACIGU
10	26	10.0	10	1	TMOF_AEDAE
11	26	10.0	15	1	PRP_MYCBO
12	26	10.0	18	1	A2M_OCTVU
13	26	10.0	19	1	NDO6_SOLTU
14	26	10.0	23	1	MDH_TREAL
15	26	10.0	25	1	ATPQ_SPTOL
16	26	10.0	25	1	H2B1_ECHES
17	26	10.0	27	1	OALA_VIPLE
18	25.5	9.8	24	1	LPER_STRFR
19	25	9.6	7	1	UNO8_PINPS
20	25	9.6	15	1	NDO8_SOLTU
21	25	9.6	20	1	FIBB_ELEMA
22	25	9.6	20	1	OALA_CROAT
23	25	9.6	20	1	PYRR_PYRAP
24	25	9.6	25	1	AU51_LITRA
25	25	9.6	25	1	AU52_LITRA
26	24.5	9.4	24	1	GYRA_STRSH
27	24.5	9.4	21	1	COXC_THUOB
28	24	9.2	13	1	CXA2_CONGE
29	24	9.2	13	1	TP13_PHYRO
30	24	9.2	14	1	MY14_PHEVI
31	24	9.2	15	1	MK1_PALPR
32	24	9.2	16	1	CXA2_CONMA
33	24	9.2	17	1	APID_BOMPA

34 24 9-2 18 1 UC21_MAIZE
35 23.5 9.0 27 1 GRP_CHICK
36 23 8.8 9 1 TKCL_CALVO
37 23 8.8 10 1 BPP_VIPAS
38 23 8.8 10 1 COXO_THUOB
39 23 8.8 15 1 AH2_PRUSE
40 23 8.8 15 1 YAA3_RHOPA
41 23 8.8 16 1 LPHI_ECOLI
42 23 8.8 16 1 PA2_NAJSP
43 23 8.8 17 1 EFG_THEAQ
44 23 8.8 18 1 RL24_PROVU
45 23 8.8 19 1 FIBB_PIG

P80627 zea mays (m
P01295 gallus gall
P41517 calliphora
P31351 vipera aspi
P80982 thunnus obe
P29260 thunnus sero
Q02006 rhodopsu
P03058 escherichia
Q10756 najia sputat
C01697 thermus aqu
P20032 proteus vul
P14477 sus scrofa

ALIGNMENTS

RESULT 1

IBP4_PIG
ID IBP4_PIG STANDARD: PRT; 16 AA.
AC P24854;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Insulin-like growth factor binding protein 4 (IGFBP-4) (IBP-4)
DE (IGF-binding protein 4) (Fragment).
GN IGFBP4.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92109718; PubMed=1723398;
RA Coleman M.E., Pan Y.-C.E., Ethernan T.D.;
RT "Identification and NH2-terminal amino acid sequence of three
RT insulin-like growth factor-binding proteins in porcine serum.";
RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
CC -!- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: CONTAINS 1 THYROGLOBULIN TYPE-I DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY.
DR PIR: JH0517; JH0517.
DR InterPro: IPR000867; IGFBP.
DR InterPro: IPR000716; Thyroglobulin_1.
DR PROSITE: PS00222; IGF-BINDING; PARTIAL.
DR PROSITE: PS00484; THYROGLOBULIN_1; PARTIAL.
KW Growth factor binding.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1799 MW; 4098884009655E2 CRC64;

Query Match 11.5%; Score 30; DB 1; Length 16;
Best Local Similarity 71.4%; Pred. NO. 5.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 39 PPPSQGK 45

Db 7 PPPSEK 13

RESULT 2

ACHD_ELEEL STANDARD: PRT; 26 AA.
ID ACHD_ELEEL
AC P09691;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Acetylcholine receptor protein, delta chain (Fragment).

OS Electrophorus electricus (Electric eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Gymniformes; Electrophoridae; Electrophorus.
 OX NCBI_TaxID=8005;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83065199; PubMed=6959131;
 RA Conti-Tronconi B.M., Hunkapiller M.W., Lindstrom J.M., Raftery M.A.;
 RT "Subunit structure of the acetylcholine receptor from Electrophorus
 electricus".
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6489-6493(1982).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
 CC DELTA, AND GAMMA CHAINS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
 DR PIR: D27262; D27262.
 DR InterPro: IPR001175; Neur_chan.
 DR Pfam: PF02931; Neur_chan_LBD; 1.
 DR PROSITE: PS00236; NEUROTR_ION_CHANNEL; PARTIAL.
 KW Receptor; Postsynaptic membrane; Ionic channel; Transmembrane.
 FT NON_TER 26 26
 SQ SEQUENCE 26 AA; 3242 MW; 8393596A49A32039 CRC64;

Query Match 11.5%; Score 30; DB 1; Length 26;
 Best Local Similarity 38.5%; Pred. No. 9.3e+02;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 19 RTQDENPVVHFVK 31
 I : : : : :
 DB 1 RNEERLINHLFK 13

RESULT 3

ID RS19_PPNWP STANDARD; PRT; 14 AA.
 AC Q52093;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 30S ribosomal protein S19 (Fragment).
 GN RPS19.
 OS Pigeon pea witches'-broom phytoplasma.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Acholeplasmataceae; Phytoplasma.
 OX NCBI_TaxID=37700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94350802; PubMed=8071198;
 RA Gunderson D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
 RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
 RT their classification".
 RL J. Bacteriol. 176:5244-5254(1994).
 CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
 CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.

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DR EMBL: L27036; AAA83946.1; -.
 DR InterPro: IPR002222; RIBOSOMAL_S19.
 DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.

KW Ribosomal protein; rRNA-binding.
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA; 1668 MW; 8FD46F6B830DFB8A CRC64;

 Query Match 10.8%; Score 28; DB 1; Length 14;
 Best Local Similarity 41.2%; Pred. No. 8.4e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 6; Gaps 1;
 OY 17 HGRTODENPVVHFVKNI 33
 I : : : : :
 DB 2 HGRTKDSK-----KNI 12

 RESULT 4
 ID DNIV_BPD10 STANDARD; PRT; 22 AA.
 AC Q38199;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE DNA-invertase (Fragment).
 GN GIN.
 OS Bacteriophage D108.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
 OX NCBI_TaxID=10671;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87316928; PubMed=2957646;
 RA Szatmari G.B., Lapointe M., Dubow M.S.;
 RT "The right end of transposable bacteriophage D108 contains a 520 base
 RT pair protein-encoding sequence not present in bacteriophage Mu.";
 RL Nucleic Acids Res. 15:6691-6703(1987).
 CC -1- FUNCTION: THIS PROTEIN CATALYZES THE INVERSION OF A 3000-BP
 CC SEGMENT OF PHAGE DNA. THE INVERSION RESULTS IN A MODIFICATION OF
 CC THE 3' END OF THE TAIL FIBER GENE AND ALTERS THE HOST SPECIFICITY.
 CC -1- SIMILARITY: BELONGS TO THE "RESOLVASE" FAMILY OF SITE-SPECIFIC
 CC RECOMBINASES.

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DR EMBL: X05926; CAA29365.1; -.
 DR InterPro: IPR001822; Recombinase.
 DR PROSITE: PS00397; RECOMBINASES_1; PARTIAL.
 DR PROSITE: PS00398; RECOMBINASES_2; PARTIAL.
 KW DNA recombination; DNA integration; DNA-binding; DNA invertase.
 FT NON_TER 1 1
 FT DNA_BIND <1 5 H-T-H MOTIF (PROBABLE).
 SQ SEQUENCE 22 AA; 2748 MW; 097E607032767C38 CRC64;

Query Match 10.8%; Score 28; DB 1; Length 22;
 Best Local Similarity 57.1%; Pred. No. 1.4e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 HPARTAH 8
 I : : : :
 DB 4 HPAKETH 10

RESULT 5

ID AMP3_MELGA STANDARD; PRT; 25 AA.
 AC P80393;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Antimicrobial peptide THP3 (Turkey heterophil peptide 3) (Fragment).
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 OX NCBI_TaxID=9103;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95053386; PubMed=7964174;
 RA Evans E.W., Beach G.G., Wunderlich J., Harmon B.G.;
 RT "Isolation of antimicrobial peptides from avian heterophils.";
 RL J. Leukoc. Biol. 56:661-665(1994).
 CC -!- FUNCTION: BACTERICIDAL ACTIVITY; INHIBITS STAPHYLOCOCCUS AUREUS.
 KW Antibiotic.
 FT NON_TER 25 25
 SQ SEQUENCE 25 AA; 2592 MW; 4AAB9AC193874035 CRC64;

Query Match 10.8%; Score 28; DB 1; Length 25;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 6; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

OY 6 TAYHGSPLQKSH 17
 | | | | |
 DB 7 TCHFGRCP--SH 16
 | | | | |

RESULT 6
 DURC_STRGP STANDARD; PRT; 19 AA.
 AC P36503;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lantibiotic duramycin C.
 OS Streptomyces griseolutes.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=29306;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=R2107;
 RX MEDLINE=91107436; PubMed=2125590;
 RA Fredenhagen A., Fendrich G., Markl F., Markl W., Gruner J.,
 RA Raschdorf F., Peter H.H.;
 RT "Duramycins B and C, two new lanthionine containing antibiotics as
 RT inhibitors of phospholipase A2. Structural revision of duramycin and
 RT cinnamycin.";
 RL J. Antibiot. 43:1403-1412(1990).
 RN [2]
 RP STRUCTURE BY NMR.
 RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;
 RT "Solution structure of the lantibiotics duramycin B and C.";
 RL (In) Schneider C.H., Eberies A.N. (eds.);
 RL Peptides 1992, pp.519-520, Escom Science Publishers, Leiden (1993).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=93387292; PubMed=8375380;
 RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;
 RT "Solution structures of the lantibiotics duramycin B and C.";
 RL Eur. J. Biochem. 216:419-428(1993).
 CC -!- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
 CC -!- FUNCTION: MATURATION OF LANTIBIOTICS INVOLVES THE ENZYMIC CONVERSION OF
 CC THR, SER, AND CYS INTO DEHYDRATED AA AND THE FORMATION OF SULFIDE
 CC BRIDGES. THIS IS FOLLOWED BY THE MEMBRANE TRANSLOCATION AND
 CC CLEAVAGE OF THE MODIFIED PRECURSOR.
 CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
 KW Antibiotic; Bacteriocin; Lantibiotic.
 FT MOD_RES 4 4 D-ALANINE.
 FT MOD_RES 6 6 D-ALANINE (BONDED TO 19).
 FT MOD_RES 11 11 D-ABU (AMINOBUTYRIC ACID).
 FT MOD_RES 18 18 D-ABU (AMINOBUTYRIC ACID).
 FT MOD_RES 19 19 LYSINOALANINE (BONDED TO 6).
 FT MOD_RES 1 18 ABU-S-CYS (METHYLLANTHIONINE).
 FT THIOETH

FT THIOETH 4 14 ALA-S-CYS (LANTHIONINE).
 FT THIOETH 5 11 ABU-S-CYS (METHYLLANTHIONINE).
 SQ SEQUENCE 19 AA; 2007 MW; E2404ECE3F95286A CRC64;

Query Match 10.4%; Score 27; DB 1; Length 19;
 Best Local Similarity 33.3%; Pred. No. 1.5e+03;
 Matches 6; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY 4 ARTAHYGLSLPOKSHGRQTQ 21
 | : | | | | |
 DB 2 ANSCSYGLTWSGDNK 19
 | : | | | | |

RESULT 7
 YOAH_KLEAE STANDARD; PRT; 20 AA.
 ID YOAH_KLEAE
 AC P56506;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein yoah (Fragment).
 GN YOAH.
 OS Klebsiella aerogenes.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=28451;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89056707; PubMed=3057324;
 RA Goncharoff P., Nichols B.P.;
 RT "Evolution of aminobenzoate synthases: nucleotide sequences of
 RT Salmonella typhimurium and Klebsiella aerogenes pabb.";
 RL Mol. Biol. Evol. 5:531-548(1988).
 RN [2]
 RP IDENTIFICATION.
 RX MEDLINE=98248213; PubMed=9588799;
 RA Rudd K.E., Humphery-Smith I., Wasinger V.C., Bairoch A.;
 RT "Low molecular weight proteins: a challenge for post-genomic
 RT research.";
 RL Electrophoresis 19:536-544(1998).
 CC -!- SIMILARITY: BELONGS TO THE UPF0181 FAMILY.
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC EMBL; M22078; ; NOT_ANNOTATED_CDS.
 DR Hypothetical protein.
 KW NON_TER 20 20
 SQ SEQUENCE 20 AA; 2270 MW; E6AF6425DD9BC88 CRC64;

Query Match 10.4%; Score 27; DB 1; Length 20;
 Best Local Similarity 38.5%; Pred. No. 1.6e+03;
 Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 9 YGSLPOKSHGRQTQ 21
 : | | | | |
 DB 2 FAGLPSLSHEQQQ 14
 : | | | | |

RESULT 8
 FLAA_TREPH STANDARD; PRT; 25 AA.
 ID FLAA_TREPH
 AC P21983;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Flagellar filament outer layer protein (Sheath protein) (Fragment).
 GN FLAA.
 OS Treponema phagedenis.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=162;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88314903; PubMed=3045083;
 RA Norris S.J., Charon N.W., Cook R.G., Fuentes M.D., Limberger R.J.;
 RT "Antigenic relatedness and N-terminal sequence homology define two
 classes of periplasmic flagellar proteins of Treponema pallidum
 subsp. pallidum and Treponema phagedenis.";
 RL J. Bacteriol. 170:4072-4082(1988).
 CC -!- FUNCTION: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.
 CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF
 REPEATING UNITS OF FLAA AROUND A CORE THAT CONTAINS SEVERAL
 ANTIGENICALLY RELATED POLYPEPTIDES.
 CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
 DR PIR: B32351; B32351
 KW Flagella; Periplasmic.
 FT NON-TER 25
 SQ SEQUENCE 25 AA; 2676 MW; E83841091FDBDAB3 CRC64;

Query Match 10.4%; Score 27; DB 1; Length 25;
 Best Local Similarity 50.0%; Pred. No. 2.1e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 LPKSHGRQ 21
 :|:|:|
 DB 16 VPKNGMG 25

RESULT 9
 ID PRPB ACIGU STANDARD; PRT; 27 AA.
 AC P04323;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Protamine B (Sturine B) (Stellin B).
 OS Acipenser guldenstadii (Caspian sturgeon), and
 OS Acipenser stellatus (Sevruga).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
 OC Acipenseridae; Acipenser.
 OX NCBI_TaxID=7902, 7903;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=A.guldenstadii;
 RA Yulikova E.P., Evseenko L.K., Baratova L.A., Belyanova L.P.,
 RA Rybin V.K., Silaev A.B.;
 RT "The primary structure of sturine B, a protamine from Caspian
 sturgeon.";
 RL Bioorg. Khim. 2:1613-1617(1976).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=A.stellatus;
 RA Rybin V.K., Yulikova E.P.;
 RL Khim. Prirod. Soedin. 5:700-704(1979).
 CC -!- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
 SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
 SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: TESTIS.
 DR PIR: A02665; SRAPC.
 KR Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
 KW Testis; DNA condensation; Nuclear protein.
 SQ SEQUENCE 27 AA; 3707 MW; E300B4651737EC80 CRC64;

Query Match 10.2%; Score 26.5; DB 1; Length 27;
 Best Local Similarity 38.1%; Pred. No. 2.6e+03;

Matches 8; Conservative 1; Mismatches 7; Indels 5; Gaps 1;
 QY 4 ARTAHYGLPQ-----KSHGR 19
 :|:|:|
 DB 1 ARRRSSRRPQRRRRRRHGR 21

RESULT 10
 ID TMOF AEDAE STANDARD; PRT; 10 AA.
 AC P19425;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
 OS Aedes aegypti (Yellowfever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 OC Aedes.
 OX NCBI_TaxID=7159;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=VERO BRACH; TISSUE=Ovary;
 RA MEDLINE=90367888; PubMed=2394318;
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RT "Mosquito oostatic factor: a novel decapeptide modulating
 trypsin-like enzyme biosynthesis in the midgut.";
 RL FASEB J. 4:3015-3020(1990).
 RN [2]
 RP SEQUENCE.
 RC STRAIN=VERO BRACH; TISSUE=Ovary;
 RX MEDLINE=93357794; PubMed=8353526;
 RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
 RT "Mass spectrometry and characterization of Aedes aegypti trypsin
 modulating oostatic factor (TMOF) and its analogs.";
 RL Insect Biochem. Mol. Biol. 23:703-712(1993).
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
 IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
 CONCENTRATION IN THE HEMOLYPH RESULTING IN INHIBITION OF OOCYTE
 DEVELOPMENT.
 CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
 EPITHELIUM 18-24 HRS AFTER A BLOOD MEAL. SYNTHESIS PEAKS AT
 36 HRS AND STOPS AT 56 HRS.
 CC PIR: A36454; A36454.
 KW Hormone.
 FT DOMAIN 3 10 POLY-PRO.
 FT VARIANT 1 2 YD -> DY (IN TMFO(B)).
 SQ SEQUENCE 10 AA; 1047 MW; 236D0A777776DC7 CRC64;

Query Match 10.0%; Score 26; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 36 PRTPPP 41
 :|:|:|
 DB 3 PAPPPP 8

RESULT 11
 ID PRP MYCBO STANDARD; PRT; 15 AA.
 AC P80149;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Proline-rich protein (Fragment).
 OS Mycobacterium bovis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1765;
 RN [1]
 RP SEQUENCE.

RC STRAIN-BCG / PARIS 1173 P2;
 RA MEDLINE-93281750; PubMed-8506381;
 RA Romain F., Augier J., Pescher P., Marchal G.A.;
 RT "Isolation of a proline-rich mycobacterial protein eliciting delayed-
 RT type hypersensitivity reactions only in guinea pigs immunized with
 RT living mycobacteria";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5322-5326(1993).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DISEASE: IMMUNODOMINANT FOR DELAYED-TYPE HYPERSENSITIVITY
 CC REACTIONS IN GUINEA PIGS.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1612 MW; 22659F848B922773 CRC64;

Query Match 10.0%; Score 26; DB 1; Length 15;
 Best Local Similarity 54.5%; Pred. No. 1.6e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Oy 35 TP--RTPPPSQ 43
 || |||
 Db 1 TPPXPPPPQ 11

RESULT 12

AD A2M_OCTVU STANDARD; PRT; 18 AA.
 AC P30800;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-2-macroglobulin homolog (Alpha-2-M) (Fragment).
 OS Octopus vulgaris (Octopus).
 CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
 CC Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=6645;
 RN [1]
 RP SEQUENCE.

RX MEDLINE-92344633; PubMed-1379044;
 RA Thøgersen I.B., Salvesen G., Brucato F.H., Pizzo S.V., Enghild J.J.;
 RT "Purification and characterization of an alpha-macroglobulin
 RT proteinase inhibitor from the mollusc Octopus vulgaris";
 RL Biochem. J. 285:521-527(1992).

CC -1- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A
 CC UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH,
 CC CALLED THE "BAIT REGION" WHICH CONTAINS SPECIFIC CLEAVAGE SITES
 CC FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT
 CC REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH
 CC TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST
 CC LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR
 CC WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE
 CC BAIT REGION A THIOLESTER BOND IS HYDROLYZED AND MEDIATES THE
 CC COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.

CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
 CC -1- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
 CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.

DR PIR; S23971; S23971.
 DR HSP; P01024; 1C3D.
 DR InterPro: IPR001599; Alpha_2_macroglobln.
 DR Pfam: PF00207; A2M; 1
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
 KW Serine protease inhibitor; Glycoprotein; Plasma; Bait region.
 FT NON_TER 1 1
 FT THIOLEST 5 8
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2011 MW; D8D61C473D9D01C9D CRC64;

Query Match 10.0%; Score 26; DB 1; Length 18;
 Best Local Similarity 25.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Oy 23 ENPVHFEKNIV 34
 | : : : : | : : :

Db 7 EQNMINEYPNVL 18

RESULT 13
 NU06_SOLTU STANDARD; PRT; 19 AA.
 ID P80729;
 AC 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 11 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Complex I-11KD) (CI-11KD) (Fragment).
 OS Solanum tuberosum (Potato).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC STRAIN-CV. BINJUE; TISSUE=Tuber;
 RA Herz U., Grohmann L.;
 RL Submitted (DEC-1996) to the SWISS-PROT data bank.
 CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE.
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER
 CC MEMBRANE.
 CC Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 KW NON_TER 19 19
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2310 MW; ODCACEF407D79F49 CRC64;

Query Match 10.0%; Score 26; DB 1; Length 19;
 Best Local Similarity 25.0%; Pred. No. 2.1e+03;
 Matches 4; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Oy 26 VVHFFKNIVTRTPPP 41
 : : | : : : |
 Db 3 IMEFAENLILRMEDP 18

RESULT 14
 MDH_THEAL STANDARD; PRT; 23 AA.
 ID P33163;
 AC 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Malate dehydrogenase (EC 1.1.1.37) (Fragment).
 GN MDH.
 OS Thermoleophilum album.
 CC Bacteria; Green non-sulfur bacteria; Thermoleophilum.
 OX NCBI_TaxID=29539;
 RN [1]
 RP SEQUENCE.
 RC STRAIN-NM;
 RA Novotny J.F. Jr., Perry J.J.;
 RT "Characterization of the malate dehydrogenase from Thermoleophilum
 RT album NM";
 RL Arch. Microbiol. 154:304-307(1990).
 CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.
 CC PIR; A60689; A60689.
 DR InterPro: IPR001252; MDH_actsite.
 DR PROSITE: PS00068; MDH; PARTIAL.
 KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
 FT NON_TER 23 23
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2544 MW; 9B48F8218EF4F125 CRC64;

Query Match 10.0%; Score 26; DB 1; Length 23;
 Best Local Similarity 44.4%; Pred. No. 2.5e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 25 PVVHFFKNI 33
 I:|:| I:
 Db 5 PLVHAMANV 13

RESULT 15
 ID ATP0_SPIOL STANDARD; PRT; 25 AA.
 AC P80082;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE ATP synthase alpha chain, mitochondrial (EC 3.6.3.14)
 DE (Fragment).
 GN ATPA.
 OS Spinacia oleracea (Spinach).
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]

RP STRAIN=CV. MEDANTA; TISSUE=Leaf mesophyll1;
 RX MEDLINE=92209531; PubMed=1313368;
 RA Hamasur B., Glaser E.;
 RT "Plant mitochondrial F0F1 ATP synthase. Identification of the
 RT individual subunits and properties of the purified spinach leaf
 RT mitochondrial ATP synthase.";
 RL Eur. J. Biochem. 205:409-416(1992).
 CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
 CC GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY
 CC SUBUNIT.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
 CC H(+)(Out).
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
 DR PIR; S21204; S21204.
 DR InterPro; IPR000194; ATPase_alpha_beta.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
 KW ATP synthesis; CF(1); Hydrogen ion transport;
 KW Hydrolyase; ATP-binding; Mitochondrion.
 FT NON_TER 25
 SQ SEQUENCE 25 AA; 2904 MW; 1B1486EBBD1A650D CRC64;

Query Match 10.0%; Score 26; DB 1; Length 25;
 Best Local Similarity 28.6%; Pred. No. 2.8e+03;
 Matches 6; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

OY 13 POKSHGRQDENPVVHFFKNI 33
 I: I: I: I: I: I:
 Db 5 PRAAEITLLESISNFTVNI 25

RESULT 16
 ID H2BL_ECHES STANDARD; PRT; 25 AA.
 AC P13281;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Histone H2B.1 sperm (Fragment).
 OS Echinus esculentus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

OC Echinoidea; Euechinoidea; Echinacea; Echinoidae; Echinidae; Echinus.
 OX NCBI_TaxID=7648;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90126812; PubMed=2298202;
 RA Hill C.S., Thomas J.O.;
 RT "Core histone-DNA interactions in sea urchin sperm chromatin. The N-
 RT terminal tail of H2B interacts with linker DNA.";
 RL Eur. J. Biochem. 187:145-153(1990).
 CC -1- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF
 CC H2A, H2B, H3, AND H4, WHICH WRAP APPROXIMATELY 146 BP OF DNA.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE HISTONE H2B FAMILY.
 DR PIR; S07770; S07770.
 DR InterPro; IPR000558; Histone_H2B.
 DR PROSITE; PS00357; HISTONE_H2B; PARTIAL.
 KW Nuclear protein; Chromosomal protein; Nucleosome core; DNA-binding;
 KW Multigene family.
 FT NON_TER 25
 SQ SEQUENCE 25 AA; 2693 MW; 9842DD3D73A3A9EC CRC64;

Query Match 10.0%; Score 26; DB 1; Length 25;
 Best Local Similarity 43.8%; Pred. No. 2.8e+03;
 Matches 7; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

OY 35 TPRTP----PESGKG 46
 I:|:| I:|:| I:|:|
 Db 7 TKRPTKRSPOKGGK 22

RESULT 17
 ID OXLA_VIPLE STANDARD; PRT; 27 AA.
 AC P81375;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE L-amino acid oxidase (EC 1.4.3.2) (LAO) (LAO) (Fragment).
 OS Vipera lebetina (Elephant snake) (Leventine viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Macrovipera.
 OX NCBI_TaxID=8709;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Tan C.H., Ang W.C.;
 RL Submitted (MAY-1998) to the SWISS-PROT data bank.
 CC -1- FUNCTION: HAS CYTOTOXIC ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: An L-amino acid + H(2)O + O(2) = a 2-oxo acid
 CC + NH(3) + H(2)O(2).
 CC -1- COFACTOR: FAD.
 CC -1- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
 CC STRONG TO MOUSE FIG-1.
 KW Oxidoreductase; Flavoprotein; FAD; Venom.
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 3210 MW; 18DED596E0610DE7 CRC64;

Query Match 10.0%; Score 26; DB 1; Length 27;
 Best Local Similarity 40.0%; Pred. No. 3e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 22 DENPVVHFFK 31
 I:|:| I:|:|
 Db 3 DKNPLEEXFR 12

RESULT 18
 ID LPER_STRFR STANDARD; PRT; 24 AA.
 AC P45440;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Erythromycin resistance leader peptide (23S rRNA methylase leader peptide).
 OS Streptomyces fradiae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1906;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88169508; PubMed=3127381;
 RA Kamimura S., Welsblum B.;
 RT "Translational attenuation control of ermSF, an inducible resistance determinant encoding rRNA N-methyltransferase from Streptomyces fradiae".
 RT fradiae".
 RL J. Bacteriol. 170:1800-1811(1988).
 CC -!- FUNCTION: THIS PEPTIDE IS INVOLVED IN THE CONTROL MECHANISM OF THE SYNTHESIS OF THE MACROLIDE-LINCOSAMIDE-STREPTOGRAMIN B RESISTANCE PROTEIN.
 CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
 CC -----
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 CC -----
 DR EMBL; M19269; AAA26741.1;
 KW Antibiotic resistance; Leader peptide.
 SQ SEQUENCE 24 AA; 2529 MW; 756C1635F8C5F06A CRC64;

Query Match 9.8%; Score 25.5; DB 1; Length 24;
 Best Local Similarity 60.0%; Pred. No. 3.1e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
 QY 36 PRT---PPPS 42
 || |||||
 DB 10 PRAALLPPPS 19

RESULT 19
 UN06_PINPS STANDARD; PRT; 7 AA.
 AC P81675;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of needles (N141) (Fragment).
 OS Pinus pinaster (Maritime pine).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine proteins".
 RT Electrophoresis 20:1098-1108(1999).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.6, ITS MW IS: 25 KDa.
 FT NON_TER 1 1
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 823 MW; 69D7672448B5740 CRC64;

Query Match 9.6%; Score 25; DB 1; Length 7;

Best Local Similarity 80.0%; Pred. No. 1e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 9 YGSLP 13
 |||||
 DB 2 YGNLP 6
 RESULT 20
 NU08_SOLTU STANDARD; PRT; 15 AA.
 ID NU08_SOLTU
 AC P80731;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 12 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Complex I-12KD) (CI-12KD) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV, BINTJE; TISSUE=Tuber;
 RA Herz U., Grohmann L.;
 RL Submitted (DEC-1996) to the SWISS-PROT data bank.
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED TO BE UBIQUINONE.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER MEMBRANE.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1668 MW; EDC87B30AD155854 CRC64;

Query Match 9.6%; Score 25; DB 1; Length 15;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 27 VHFERNIVTP 36
 || :|||
 DB 1 VHMARNMXP 10

RESULT 21
 FIBB_ELEMA STANDARD; PRT; 20 AA.
 AC P14538;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-JAN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
 GN FGB
 OS Elephas maximus (Indian elephant).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.
 OX NCBI_TaxID=9783;
 RN [1]
 RP SEQUENCE.
 RA O'Neil P.B., Doolittle R.F.;
 RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
 RL Syst. Zool. 22:590-595(1973).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA

CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
 KW BLOOD coagulation; Plasma; Sulfation.
 FT PEPTIDE 1 20 FIBRINOPEPTIDE B.
 FT MOD_RES 4 4 SULFATION.
 FT NON_TER 20 20
 FT SEQUENCE 20 AA; 2107 MW; B4F52B9599933273 CRC64;

Query Match 9.6%; Score 25; DB 1; Length 20;
 Best Local Similarity 55.6%; Pred. No. 2.9e+03;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 36 PRTPPSQG 44
 | | | |
 DB 10 PGAVPSVG 18

RESULT 22
 OXLA_CROAT STANDARD; PRT; 20 AA.
 AC P56742;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE L-amino acid oxidase (EC 1.4.3.2) (LAO) (Apoxin 1) (Fragment).
 OS *Crotalus atrox* (Western diamondback rattlesnake).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 CC Viperidae; Crotalinae; Crotalus.
 CC NCBI_TaxID=8730;
 RN [1]
 RP SEQUENCE.

RC TISSUE-Venom;
 RX MEDLINE=97238898; PubMed=9083096;
 RA Tottli S., Naito M., Tsuruo T.;
 RT "Apoxin I, a novel apoptosis-inducing factor with L-amino acid oxidase
 RT activity purified from Western diamondback rattlesnake venom.";
 RL J. Biol. Chem. 272:9539-9542(1997).
 CC -!- FUNCTION: CATALYZES AN OXIDATIVE DEAMINATION OF PREDOMINANTLY
 CC HYDROPHOBIC AND AROMATIC L-AMINO ACIDS. HAS AN ANTIBACTERIAL
 CC EFFECT AND AN ABILITY TO INDUCE APOPTOSIS. THE H(2)O(2) PRODUCED
 CC BY L-AMINO ACID OXIDATION IS INVOLVED IN THE APOXIN-1 INDUCED
 CC APOPTOSIS AND HEMORRHAGE CAUSED BY THE VENOM.
 CC -!- CATALYTIC ACTIVITY: An L-amino acid + H(2)O + O(2) = a 2-oxo acid
 CC + NH(3) + H(2)O(2).
 CC -!- COFACTOR: FAD.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: PLASMA MEMBRANE (POTENTIAL).
 CC -!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
 CC STRONG. TO MOUSE FIG-1.
 KW Oxidoreductase; Flavoprotein; FAD; Venom; Apoptosis; Antibiotic.
 FT NON_TER 20 20
 FT SEQUENCE 20 AA; 2521 MW; 95E973C6C86588E7 CRC64;

Query Match 9.6%; Score 25; DB 1; Length 20;
 Best Local Similarity 40.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 22 DENPVHFEK 31
 | | | |
 DB 3 DRNPLEXFR 12

RESULT 23
 PYRR_PYRAP STANDARD; PRT; 20 AA.
 AC P37362; P80307;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Pyrrhocorin.
 OS Pyrrhocoris apterus (Sap sucking bug).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;
 CC Heteroptera; Panheteroptera; Pentatomomorpha; Lygaeoidea;
 CC Pyrrhocoridae; Pyrrhocoris.
 CC NCBI_TaxID=37000;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Hemolymph;
 RX MEDLINE=94271176; PubMed=8002963;
 RA Cociancich S., Dupont A., Hegy G., Lanot R., Holder F., Hetru C.,
 RA Hoffmann J.A., Bulet P.;
 RT "Novel inducible antibacterial peptides from a hemipteran insect, the
 RT sap-sucking bug *Pyrrhocoris apterus*.";
 RL Biochem. J. 300:567-575(1994).
 RN [2]
 RP CARBOHYDRATE-LINKAGE SITE THR-11.
 RX MEDLINE=99177428; PubMed=10076062;
 RA Hoffmann R., Bulet P., Urge L., Otvoes L. Jr.;
 RT "Range of activity and metabolic stability of synthetic antibacterial
 RT glycopeptides from insects.";
 RL Biochim. Biophys. Acta 1426:459-467(1999).
 CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE. AFFECTS GRAM-NEGATIVE BACTERIA
 CC E. COLI 1106, P. AERUGINOSA, E. COLI D22 AND E. CLOACAE AND
 CC GRAM-POSITIVE BACTERIA M. LUTEUS AND B. SUBTILIS.
 CC -!- PTM: O-LINKED GLYCAN CONSISTS OF A GAL-GALNAC DISACCHARIDE, O-
 CC GLYCOSYLATION IS ESSENTIAL FOR FULL BIOLOGICAL ACTIVITY.
 CC -!- SIMILARITY: TO DROSOPHILA DROSOCIN.
 DR PIR; S44465; S44465.
 KW Antibiotic; Glycoprotein; Insect immunity; Hemolymph.
 FT CARBOHYD 11 11 O-LINKED (GALNAC...).
 FT SEQUENCE 20 AA; 2341 MW; F4320EC2FE29462C CRC64;

Query Match 9.6%; Score 25; DB 1; Length 20;
 Best Local Similarity 45.5%; Pred. No. 2.9e+03;
 Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 31 KNIVTPRTPPP 41
 | | | |
 DB 3 KGSYLPRTPPP 13

RESULT 24
 AUST_LITRA STANDARD; PRT; 25 AA.
 ID AU51_LITRA
 AC P82401;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Aurein 5.1.
 OS *Litoria raniformis* (Southern bell frog), and
 OS *Litoria aurea* (green and golden bell frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 CC Litoria.
 CC NCBI_TaxID=116057, 8371;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE-Granular dorsal gland;
 RX MEDLINE=20408845; PubMed=10951191;
 RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
 RA Wallace J.C., Tyler M.J.;
 RT "The antibiotic and anticancer active aurein peptides from the
 RT Australian bell frogs *Litoria aurea* and *Litoria raniformis* the
 RT solution structure of aurein 1.2.";
 RL Eur. J. Biochem. 267:5330-5341(2000).
 CC -!- FUNCTION: HAS NO ANTIMICROBIAL OR ANTICANCER ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC SEQUENCE 25 AA; 2547 MW; 15C6169CD98AFC7 CRC64;

Query Match 9.6%; Score 25; DB 1; Length 25;
 Best Local Similarity 37.5%; Pred. No. 3.7e+03;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 32 NIVTPRTP 39
 ::: l:l
 DB 16 DVLKPKTP 23

RESULT 25

AU52_LITRA STANDARD; PRT; 25 AA.
 AC P82402;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Aurein 5.2.
 OS Litoria raniformis (Southern bell frog), and
 OS Litoria aurea (Green and golden bell frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=116057, 8371;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE-Granular dorsal gland;
 RX MEDLINE=20408845; PubMed=10951191;
 RA Rozek T., Wegener K.L., Bowle J.H., Oliver I.N., Carver J.A.,
 RA Wallace J.C., Tyler M.J.;
 RT "The antibiotic and anticancer active aurein peptides from the
 RT Australian bell frogs Litoria aurea and Litoria raniformis the
 RT solution structure of aurein 1.2.";
 RL Eur. J. Biochem. 267:5330-5341(2000).
 CC -1- FUNCTION: HAS ANTIMICROBIAL ACTIVITY AGAINST L. LACTIS AND
 CC S. UBERIS.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 KW Antibiotic.
 SQ SEQUENCE 25 AA: 2453 MW; 5CA28F10359347AC CRC64;

Query Match 9.6%; Score 25; DB 1; Length 25;
 Best Local Similarity 37.5%; Pred. No. 3.7e+03;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 32 NIVTPRTP 39
 ::: l:l
 DB 16 DVLKPKTP 23

RESULT 26

GYRA_STRSH STANDARD; PRT; 21 AA.
 AC P50071;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE DNA gyrase subunit A (EC 5.99.1.3) (Fragment).
 GN GYRA.
 OS Streptomyces sp. *sp.*
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=29307;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIB 11891;
 RX MEDLINE=93316846; PubMed=8392138;
 RA Thiera A.S., Cundliffe E.;
 RT "Expression and analysis of two gyrB genes from the novobiocin
 RT producer, Streptomyces sp. *sp.*"
 RL Mol. Microbiol. 8:495-506(1993).
 CC -1- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-
 CC STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE

CC INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
 CC DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
 CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
 CC of double-stranded DNA.
 CC -1- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA
 CC BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE
 CC ENZYME FORMS AN A2B2 TETRAMER.
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DR EMBL; 217305; CAA78953.1; -
 KW Topoisomerase; Isomerase; DNA-binding.
 FT NON_TER 21 21
 SQ SEQUENCE 21 AA: 2203 MW; 5E2F9DEA8DB83697 CRC64;

Query Match 9.4%; Score 24.5; DB 1; Length 21;
 Best Local Similarity 34.6%; Pred. No. 3.5e+03;
 Matches 9; Conservative 2; Mismatches 6; Indels 9; Gaps 2;

QY 22 DEN-PVHFVKNIPTPTPPSQGK 46
 ::: l:l
 DB 3 DENTPVM-----PEEVPVEGVG 20

RESULT 27

COXC_THUOB STANDARD; PRT; 24 AA.
 ID COXC_THUOB
 AC P80973;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome c oxidase polypeptide VA-2 (EC 1.9.3.1) (Fragment).
 OS Thunus obesus (Bigeye tuna).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OX NCBI_TaxID=8241;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Heart, and Liver;
 RX MEDLINE=97454291; PubMed=9310366;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RT "The subunit structure of cytochrome-c oxidase from tuna heart and
 RT liver.";
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -1- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
 CC OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytocrome c + O(2) -> 4 ferrocytocrome
 CC c + 2 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
 DR InterPro: IPR003204; Cyt_c_ox5a.
 KW Pfam: PF02284; COX5A; 1.
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
 FT NON_TER 24 24
 SQ SEQUENCE 24 AA: 2903 MW; 20998FB91F22E43B CRC64;

Query Match 9.4%; Score 24.5; DB 1; Length 24;
 Best Local Similarity 31.8%; Pred. No. 4e+03;
 Matches 7; Conservative 4; Mismatches 6; Indels 5; Gaps 1;

QY 16 SHGRITQ-----DENPVHFVK 32
 ::: l:l

Db 1 SHGKQETDEEDARWVTFNKS 22

RESULT 28

CXA2_CONGE STANDARD; PRT; 13 AA.

AC P01520;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alpha-conotoxin GII.

OS Conus geographus (Geography cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;

CC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI_TaxID=6491;

RN [1]

RN SEQUENCE.

RX MEDLINE=81191854; PubMed=7014556;

RA Gray W.R., Luque A., Olivera B.M., Barrett J., Cruz L.J.;

RT "Peptide toxins from Conus geographus venom.";

RL J. Biol. Chem. 256:4734-4740(1981).

RN [2]

RN DISULFIDE BONDS.

RX MEDLINE=84032400; PubMed=6630187;

RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;

RT "Conotoxin MI. Disulfide bonding and conformational states.";

RL J. Biol. Chem. 258:12247-12251(1983).

RN [3]

RN REVIEW.

RX MEDLINE=89024586; PubMed=3052286;

RA Gray W.R., Olivera B.M., Cruz L.J.;

RT "Peptide toxins from venomous Conus snails.";

RL Annu. Rev. Biochem. 57:665-700(1988).

CC -!- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS INHIBIT THEM.

CC -!- SUBCELLULAR LOCATION: Secreted

CC -!- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.

DR PIR: A01783; NTKN2G.

DR HSPG; P01519; INOT.

KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation; Venom.

FT DISULFID 2 7

FT DISULFID 3 13

FT MOD_RES 13 13

FT SEQUENCE 13 AA; 1422 MW; DEE831C39297EED CRC64;

Query Match 9.2%; Score 24; DB 1; Length 13;

Best Local Similarity 50.0%; Pred. No. 2.4e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 HPARTAHY 9

Db [1] :

Db 4 HPACGKHF 11

RESULT 29

TP13_PHYRO STANDARD; PRT; 13 AA.

AC P04056;

DT 01-NOV-1986 (Rel. 03, Created)

DT 01-NOV-1986 (Rel. 03, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Tryptophyllin-13.

OS Phyllomedusa rohdei (Rohde's leaf frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

CC Phyllomedusa.

OX NCBI_TaxID=8394;

RN [1]

RN SEQUENCE.

RA Montecucchi P.C., Gozzini L., Erspamer V.;

RT "Primary structure determination of a tryptophan-containing tridecapeptide from Phyllomedusa rohdei.";

RL Int. J. Pept. Protein Res. 27:175-182(1986).

CC -!- TISSUE SPECIFICITY: SECRETED.

DR PIR: A05174; A05174.

KW Amphibian skin.

FT MOD_RES 1 1

FT SEQUENCE 13 AA; 1646 MW; 33BF33A212227773 CRC64;

Query Match 9.2%; Score 24; DB 1; Length 13;

Best Local Similarity 66.7%; Pred. No. 2.4e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 36 PRTPPP 41

Db [1] :

Db 4 PYWPPP 9

RESULT 30

MY14_PHEVI STANDARD; PRT; 14 AA.

AC P46980;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Myoactive tetradecapeptide (PTP).

OS Pheretima vittata (Earthworm).

OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;

OC Lumbricina; Megascolecidae; Pheretima.

OX NCBI_TaxID=46674;

RN [1]

RN SEQUENCE, AND SYNTHESIS.

RC TISSUE=Gut;

RX MEDLINE=96087879; PubMed=8532604;

RA Okena K., Oumi T., Matsushima O., Ikeda T., Fujita T., Minakata H., Nomoto K.;

RT "A novel gut tetradecapeptide isolated from the earthworm, Eisenia foetida.";

RL Peptides 16:995-999(1995).

CC -!- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT MUSCLES.

CC -!- SIMILARITY: TO INSECTS ALLATOTROPIN.

KW Neuropeptide; Amidation.

FT MOD_RES 14 14

FT SEQUENCE 14 AA; 1522 MW; DA40BE67CCD91AD CRC64;

Query Match 9.2%; Score 24; DB 1; Length 14;

Best Local Similarity 55.6%; Pred. No. 2.6e+03;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 10 GSIPKSHG 18

Db [1] :

Db 5 GSADRIHG 13

RESULT 31

MK1_PALPR STANDARD; PRT; 15 AA.

AC P80408;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Metalinikowin I.

OS Palomena prasina.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

CC Pterygota; Neoptera; Paraneoptera; Hemiptera; Euhemiptera;

OC Heteroptera; Panheteroptera; Pentatomomorpha; Pentatomoidea;

OC Pentatomidae; Palomena.

OX NCBI_TaxID=55431;

RN [1]

RN SEQUENCE.

RC TISSUE=Hemolymph;
 RA Chernysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 RT Palomera prasina. Identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin."
 RL J. Insect Physiol. 42:81-89(1996).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
 CC BACTERIA.
 CC -1- INDUCTION: BY BACTERIAL INFECTION.
 KW Antibiotic; Insect immunity.
 SQ SEQUENCE 15 AA: 1838 MW; 21407E663CE46299 CRC64;

Query Match 9.2%; Score 24; DB 1; Length 15;
 Best Local Similarity 57.1%; Pred. No. 2.8e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 36 PRTPPPS 42
 || ||
 Db 8 PRPRPN 14

RESULT 32
 CXA2_CONMA STANDARD; PRT; 16 AA.
 ID CXA2_CONMA
 AC P56636;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-conotoxin MII (M2).
 OS Conus magus (Magus cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 RX NCBI_TaxID=6492;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RC TISSUE=Venom.
 RX MEDLINE=96205934; PubMed=8631783;
 RA Cartier G.E., Yoshikami D., Gray W.R., Luo S., Olivera B.M.,
 RA McIntosh J.M.;
 RT "A new alpha-conotoxin which targets alpha3beta2 nicotinic
 RT acetylcholine receptors."
 RL J. Biol. Chem. 271:7522-7528(1996).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=98062282; PubMed=9398298;
 RA Shon K.-J., Koerber S.C., Rivier J.E., Olivera B.M., McIntosh J.M.;
 RT "Three-dimensional solution structure of alpha-conotoxin MII, an
 RT alpha3beta2 neuronal nicotinic acetylcholine receptor-targeted
 RT ligand."
 RL Biochemistry 36:15693-15700(1997).
 RN [3]

RP STRUCTURE BY NMR.
 RX MEDLINE=99060038; PubMed=9843366;
 RA Hill J.M., Oomen C.J., Miranda L.P., Bingham J.-P., Alewood P.F.,
 RA Craik D.J.;
 RT "Three-dimensional solution structure of alpha-conotoxin MII by NMR
 RT spectroscopy: effects of solution environment on helicity."
 RL Biochemistry 37:15621-15630(1998).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
 CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 SUBUNITS. IT
 CC HAS AN ACTIVITY 2 TO 4 ORDERS OF MAGNITUDE LESS POTENT ON OTHER
 CC NACHR SUBUNIT COMBINATIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
 DR PDB; IM2; 21-OCT-98.
 KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
 KW Venom; 3D-structure.
 FT DISULFID 8
 2
 3 16

FT MOD_RES 16 16 AMIDATION.
 SQ SEQUENCE 16 AA: 1716 MW; 282AEF190166CAF9 CRC64;
 Query Match 9.2%; Score 24; DB 1; Length 16;
 Best Local Similarity 80.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 24 NPVVH 28
 ||||
 Db 5 NPVCH 9

RESULT 33
 APID_BOMPA STANDARD; PRT; 17 AA.
 ID APID_BOMPA
 AC P81464;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Apidaecin.
 OS Bombus pascuorum.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoidea; Aculeata;
 CC Apoidea; Apidae; Bombus.
 RX NCBI_TaxID=65598;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RX MEDLINE=97362903; PubMed=9219367;
 RA Rees J.A., Monlatte M., Bulet P.;
 RT "Novel antibacterial peptides isolated from a European bumblebee,
 RT Bombus pascuorum (Hymenoptera, Apoidea)."
 RL Insect Biochem. Mol. Biol. 27:413-422(1997).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
 CC BACTERIA.
 CC -1- INDUCTION: BY BACTERIAL INFECTION.
 KW Insect immunity; Antibiotic; Hemolymph.
 SQ SEQUENCE 17 AA: 1963 MW; CD1D0D02C8BC23D1 CRC64;

Query Match 9.2%; Score 24; DB 1; Length 17;
 Best Local Similarity 55.6%; Pred. No. 3.2e+03;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 33 IVTPRTPPP 41
 | |||||
 Db 7 IPPRPPHP 15

RESULT 34
 UC21_MAIZE STANDARD; PRT; 18 AA.
 ID UC21_MAIZE
 AC P80627;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 443)
 DE (Fragment).
 OS Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 CC Panicoideae; Andropogoneae; Zea.
 RX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 5.9, ITS MW IS: 26.5 kDa.
 CC -!- SIMILARITY: TO L-ASCORBATE PEROXIDASES.
 DR HSP: P48534; LAPX.
 DR Maize-2DPAGE: P80627; COLEOPTILE.
 DR MaizeDB: 123953; -.
 FT NON_TER 1 18
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1938 MW; F32F6FEF038BAB8A CRC64;

Query Match 9.2%; Score 24; DB 1; Length 18;
 Best Local Similarity 25.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 HHPARTAHYGSLPQKS 16
 Db 3 NYPTVSAEYSXAVEKA 18
 : : | : | : | :
 : : | : | : | :
 : : | : | : | :

RESULT 35
 GRP_CHICK STANDARD; PRT; 27 AA.
 AC P01295;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Gastrin-releasing peptide (GRP) (Proventricular peptide) [Contains:
 DE Neuromedin C (GRP-10)].
 GN GRP.

OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81164953; PubMed=7215543;
 RA McDonald T.J., Joernvall H., Ghatei M., Bloom S.R., Mutt V.;
 RT "Characterization of an avian gastric (proventricular) peptide having
 RT sequence homology with the porcine gastrin-releasing peptide and the
 RT amphibian peptides bombesin and aiylesin.";
 RL FEBS Lett. 122:45-48(1980).
 RN [2]
 RP SEQUENCE.

RX MEDLINE=9012926; PubMed=2297533;
 RA Campbell B.J., Young J., Dimaline R., Dockray G.J.;
 RT "Isolation, sequence and biosynthetic significance of a novel
 RT fragment of gastrin-releasing peptide from chicken proventriculus.";
 RL Biochim. Biophys. Acta 1048:66-71(1990).
 CC -!- FUNCTION: GRP stimulates gastrin release as well as other
 CC gastrointestinal hormones.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
 CC FAMILY

DR PIR; A01563; RHCHA.
 DR PIR; S08150; S08150.
 DR InterPro; IPR000874; Bombesin.
 DR Pfam; PF02044; Bombesin; 1.
 DR PROSITE; PS00257; BOMBESIN; 1.
 KW Bombesin family; Amidation.
 FT PEPTIDE 18 27 NEUROMEDIN C.
 FT MOD_RES 27 27 AMIDATION.
 FT MOD_RES 27 27
 SQ SEQUENCE 27 AA; 2842 MW; 3C121D0118D551C7 CRC64;

Query Match 9.0%; Score 23.5; DB 1; Length 27;
 Best Local Similarity 45.7%; Pred. No. 6.1e+03;
 Matches 7; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

OY 3 PARTAHYGSLSLPQKS 17
 Db 9 PALTKYI---PRGSH 20

RESULT 36
 TKCL_CALVO STANDARD; PRT; 9 AA.
 AC P41517;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Callitachykinin I.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestroidea; Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.

RX MEDLINE=95075727; PubMed=7984492;
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
 RA Naessel D.R.;
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from
 RT the blowfly, Calliphora vomitoria, that have resemblances to
 RT tachykinins.";
 RL Peptides 15:761-768(1994).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE.
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 9 9
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 981 MW; 2417C86B59CDC1B7 CRC64;

OY 4 ARTAHYG 10
 Db 1 APTAFYG 7
 | | | | | | | | | |
 | | | | | | | | | |

Query Match 8.8%; Score 23; DB 1; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1e+05;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 37
 BPP_VIPAS STANDARD; PRT; 10 AA.
 AC P31351;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting
 DE enzyme inhibitor).
 OS Vipera aspis (Aspic viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Vipera.
 OX NCBI_TaxID=8706;
 RN [1]
 RP SEQUENCE.

RX TISSUE-Venom;
 RX MEDLINE=90382616; PubMed=2169439;
 RA Komori Y., Sugihara H.;
 RT "Characterization of a new inhibitor for angiotensin converting
 RT enzyme from the venom of Vipera aspis aspis.";
 RL Int. J. Biochem. 22:767-771(1990).
 CC -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
 CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
 CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
 DR PIR; A60377; XASNPC.
 KW Hypotensive agent; Venom.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 8.8%; Score 23; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 2.4e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 36 PRTTP 40

DB 6 PKVPP 10

RESULT 38

COXO_THUOB

ID COXO_THUOB STANDARD; PRT; 10 AA.

AC P80982;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).

OS Thunus obesus (Bigeye tuna).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;

OC Scombridae; Thunnus.

OC NCBI_TaxID=8241;

RN [1]

RP SEQUENCE.

RC TISSUE=Heart, and Liver;

RX MEDLINE=97454291; PubMed=9310366;

RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,

RA Kadenbach B.;

RT "The subunit structure of cytochrome-c oxidase from tuna heart and

RT liver.";

RL Eur. J. Biochem. 248:99-103(1997).

CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE

CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN

CC MITOCHONDRIAL ELECTRON TRANSPORT.

CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome

CC c + 2 H(2)O.

CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.

CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.

KW Oxidoreductase; Inner membrane; Mitochondrion.

FT NON_TER 10 10

FT SEQUENCE 10 AA; 1059 MW; 126DE767687B1DCB CRC64;

Query Match

Best Local Similarity 8.8%; Score 23; DB 1; Length 10;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 7 AHYGLSPKKS 16

DB 1 SHYAGPGKN 10

RESULT 39

AH2_PRUSE

ID AH2_PRUSE STANDARD; PRT; 15 AA.

AC P29260;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Amygdalin beta-glucosidase I' (EC 3.2.1.117) (Amygdalin hydrolase

DE isozyme I') (AH I') (Fragment).

OS Prunus serotina (Black cherry).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermaphyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.

OC NCBI_TaxID=23207;

RN [1]

RP SEQUENCE.

RC TISSUE=Seed;

RA Li C.P., Swain E., Poulton J.E.;

RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";

RL Plant Physiol. 100:282-290(1992)

CC -1- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-

CC glucose.

CC -1- SUBUNIT: MONOMER.

CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS

CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON

CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR

CC EMBRYONAL TISSUES.

CC -1- PTM: GLYCOSYLATED.

KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.

FT NON_TER 15 15

FT SEQUENCE 15 AA; 1650 MW; F7CC4FA321E12EC4 CRC64;

Query Match

Best Local Similarity 8.8%; Score 23; DB 1; Length 15;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 24 NPVVHF 29

DB 4 DPPIHF 9

RESULT 40

YAA3_RHOPA

ID YAA3_RHOPA STANDARD; PRT; 15 AA.

AC Q02006;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein in AADR 3'region (Fragment).

OS Rhodopseudomonas palustris.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Bradyrhizobium group; Rhodopseudomonas.

OC NCBI_TaxID=1076;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CGA009;

RX MEDLINE=92394882; PubMed=1522059;

RA Dispensa M., Thomas C.T., Kim M.K., Perrotta J.A., Gibson J.,

RA Harwood C.S.;

RT "Anaerobic growth of Rhodopseudomonas palustris on 4-hydroxybenzoate

RT is dependent on Aadr, a member of the cyclic AMP receptor protein

RT family of transcriptional regulators.";

RL J. Bacteriol. 174:5803-5813(1992).

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CC EMBL; M92426; AAA26091.1; -

DR PIR; C43334; C43334.

DR Hypothetical protein.

FT NON_TER 15 15

FT SEQUENCE 15 AA; 1926 MW; 149B01A548D7C202 CRC64;

Query Match

Best Local Similarity 8.8%; Score 23; DB 1; Length 15;

Matches 5; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

OY 21 QDENPW----HFF 30

DB 2 ROETPAYLRARHYF 15

RESULT 41

LPHI_ECOLI

ID LPHI_ECOLI STANDARD; PRT; 16 AA.

AC P03058;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE His operon leader peptide (Attenuator peptide).
GN HISL OR B2018 OR STM2070.1.
OS Escherichia coli, and
OC Salmonella typhimurium.
CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Escherichia.
ON NCBI_TaxID=562, 602;
RX [1]
RP SEQUENCE FROM N.A.
RC SPECIES-E.coli, and S.typhimurium; STRAIN=K12, AND LT2;
RX MEDLINE=89094829; PubMed=3062174;
RA Carlomagno M.S., Chiariotti L., Alfano P., Nappo A.G., Bruni C.B.;
RT "Structure and function of the Salmonella typhimurium and Escherichia
col K-12 histidine operons.";
RL J. Mol. Biol. 203:585-606(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-E.coli;
RX MEDLINE=82059525; PubMed=6170941;
RA Verde P., Frunzio R., di Nocera P.P., Blasi F., Bruni C.B.;
RT "Identification, nucleotide sequence and expression of the regulatory
region of the histidine operon of Escherichia coli K-12.";
RL Nucleic Acids Res. 9:2075-2086(1981).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-E.coli;
RX MEDLINE=79033821; PubMed=360215;
RA Dinocera P.P., Blasi F., Dilauro R., Frunzio R., Bruni C.B.;
RT "Nucleotide sequence of the attenuator region of the histidine operon
of Escherichia coli K-12.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:4276-4280(1978).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-E.coli;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES-S.typhimurium; STRAIN=LT2;
RX MEDLINE=79033822; PubMed=360216;
RA Barnes W.M.;
RT "DNA sequence from the histidine operon control region: seven
histidine codons in a row.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:4281-4285(1978).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES-S.typhimurium; STRAIN=LT2;
RA Barnes W.M., Husson R.N., Whittier R.;
RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES-S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of salmonella enterica serovar typhimurium
LT2.";
RL Nature 413:852-856(2001).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN THE ATTENUATION MECHANISM
CC FOR THE CONTROL OF THE EXPRESSION OF THE HIS STRUCTURAL GENES.
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CC EMBL; V00285; CAA23550.1; .
CC DR EMBL; V00284; CAA23548.1; .
CC DR EMBL; X13462; CAA31810.1; .
CC DR EMBL; V01371; CAA24656.1; .
CC DR EMBL; AE000293; AAC75079.1; .
CC DR EMBL; X13464; CAA31821.1; .
CC DR EMBL; J01804; AAA8613.1; .
CC DR EMBL; AE008791; .; NOT_ANNOTATED_CDS.
CC DR PIR; A03394; LFECB.
CC DR EcoGene; EG11269; hisL.
CC DR StyGene; SGI0166; hisL.
CC KW Histidine biosynthesis; Leader peptide; Complete proteome.
CC SQ SEQUENCE 16 AA; 2081 MW; C8B7907BF6283BBA CRC64;

Query Match 8.8%; Score 23; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHP 3
Db 13 HHP 15

RESULT 42
PA2_NAJSP
ID PA2_NAJSP STANDARD; PRT; 16 AA.
AC Q10756;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase)
DE (Muscarinic inhibitor) (Fragment).
DE Naja sputatrix (Malayan spitting cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Serpentes; Colubroidae;
OC Elapidae; Elapinae; Naja.
CC NCBI_TaxID=33626;
CC [1]
CC SEQUENCE.
CC TISSUE-Venom;
CC MEDLINE=96195757; PubMed=8638927;
CC Miyoshi S.-I., Iu A.T.;
CC "Phospholipase A2 from Naja sputatrix venom is a muscarinic
CC acetylcholine receptor inhibitor.";
CC Arch. Biochem. Biophys. 328:17-25(1996).
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-
CC ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES. BLOCKS NEUROMUSCULAR
CC TRANSMISSION AT THE POSTSYNAPTIC SITE. BINDS TO THE MUSCARINIC
CC ACETYLCHOLINE RECEPTOR.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
CC HSP: P00598; IPOB.
CC InterPro: IPR001211; PLP.A2.
CC Pfam: PF00068; Phoslip; 1.
CC PROSITE: PS00118; PA2_HIS; PARTIAL.
CC PROSITE: PS00119; PA2_ASP; PARTIAL.
CC Hydrolase; Lipid degradation; Calcium; Venom; Neurotoxin;
CC Presynaptic neurotoxin; Postsynaptic neurotoxin.
CC NON_TER 16
CC SQ SEQUENCE 16 AA; 1969 MW; 9AC1F9834BB585F0 CRC64;

Query Match 8.8%; Score 23; DB 1; Length 16;

Best Local Similarity 40.0%; Pred. No. 4e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 30 FKNIVTPRTP 39
| | | | |
Db 5 FKNVIQCTVP 14

RESULT 43

EFQ_THEAQ STANDARD; PRT; 17 AA.
AC Q01697;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Elongation factor G (EF-G) (Fragment).
GN FUSA OR FUS.

OS Thermus aquaticus.
OC Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.

OX NCBI_TaxID=271;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP 00276;
RX MEDLINE=92362620; PubMed=1499561;
RA Voss R.H., Hartmann R.K., Lippmann C., Alexander C., Jahn O., Erdmann V.;

RT "Sequence of the tufA gene encoding elongation factor EF-Tu from
RT Thermus aquaticus and overproduction of the protein in Escherichia
RT coli.";

RL Eur. J. Biochem. 207:839-846(1992).

CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
CC OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
CC RIBOSOME.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.

CC EF-G/EF-2 SUBFAMILY.

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CC or send an email to license@isb-sib.ch).

DR EMBL; X66322; CAA46997.1; -.

DR PIR; S29294; S29294.

DR HSP; P13551; LDAR.

DR InterPro: IPR000795; GTP_EFTU.

DR PROSITE; PS00301; EFATOR_GTP; PARTIAL.

KW Elongation factor; Protein biosynthesis; GTP-binding.

FT NON_TER 1

SQ SEQUENCE 17 AA; 2094 MW; EA66E0F5F86E1D CRC64;

Query Match 8.8%; Score 23; DB 1; Length 17;
Best Local Similarity 37.5%; Pred. No. 4.3e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 HYGSLPQK 15
| | | | |
Db 1 HYGVPVPRQ 8

RESULT 44

RL24_PROVU STANDARD; PRT; 18 AA.
AC P20032;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE 50S ribosomal protein L24 (Fragment).

GN RPLX.

OS Proteus vulgaris.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=585;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89125589; PubMed=2464692;
RA Cerretti D.P., Mattheakis L.C., Kearney K.R., Vu L., Nomura M.;

RT "Translational regulation of the spc operon in Escherichia coli.

RT Identification and structural analysis of the target site for S8

RT repressor protein.";

RL J. Mol. Biol. 204:309-329(1988).

CC -1- FUNCTION: THIS PROTEIN IS FOUND IN THE RIBONUCLEOPROTEIN CORE AND

CC IS INVOLVED IN THE EARLY ASSEMBLY OF THE 50S SUBUNIT. IT IS NOT

CC INVOLVED IN THE FUNCTIONS OF THE MATURE 50S SUBUNIT.

CC -1- SIMILARITY: BELONGS TO THE L24P FAMILY OF RIBOSOMAL PROTEINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).

DR EMBL; X36264; AAA25661.1; -.

DR InterPro: IPR000302; Ribosomal_L24_NusG.

DR PROSITE; PS01108; RIBOSOMAL_L24; PARTIAL.

KW Ribosomal protein.

FT NON_TER 1

SQ SEQUENCE 18 AA; 2202 MW; 43606F53C5CBA57C CRC64;

Query Match 8.8%; Score 23; DB 1; Length 18;
Best Local Similarity 36.4%; Pred. No. 4.5e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 22 DENPVVHFKN 32

| | | | |

Db 2 EDGKVRFFKS 12

RESULT 45

FIBB_PIG

ID FIBB_PIG STANDARD; PRT; 19 AA.

AC P14477;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).

GN FGB.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE.

RA Blomback B., Blomback M., Grondahl N.J.;

RT "Studies on fibrinopeptides from mammals."

RL Acta Chem. Scand. 19:1789-1791(1965).

CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT

CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET

CC AGGREGATION.

CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS

CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY

CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA

CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES

CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

DR InterPro: IPR002181; Fibrinogen_C.

DR PROSITE; PS00514; FIBRIN_AG_DOMAIN; PARTIAL.

KW Blood coagulation; Plasma; Sulfation.

FT PEPTIDE 1 19 FIBRINOPEPTIDE B.

FT MOD.RES 4 4 Sulfation.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2200 MW; 09F87E44F4F3863D CRC64;

Query Match 8.8%; Score 23; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 4.8e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 21 QDENPVVH 28
 . | | |
 Db 8 EDGRPKVH 15

Search completed: September 23, 2002, 11:11:07
 Job time: 130 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 23, 2002, 11:08:56 ; Search time 23.92 Seconds
 (without alignments)
 332.683 Million cell updates/sec

Title: US-09-813-383-1
 Perfect score: 260
 Sequence: 1 HHPARTAHYGLSPKSHGRT.....VHFFKNIVTPPTPPSQKRG 46

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 11731

Minimum DB seq length: 0
 Maximum DB seq length: 27

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL19:*
 1: sp_archaea:*
 2: sp_bacteria:*
 3: sp_fungi:*
 4: sp_human:*
 5: sp_invertebrate:*
 6: sp_mammal:*
 7: sp_mhc:*
 8: sp_organelle:*
 9: sp_phase:*
 10: sp_plant:*
 11: sp_rodent:*
 12: sp_virus:*
 13: sp_vertebrate:*
 14: sp_unclassified:*
 15: sp_fvrius:*
 16: sp_bacteriap:*
 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	13.5	10	12	Q900X9 polyomaviru
2	35	13.5	10	12	Q900X5 polyomaviru
3	35	13.5	10	12	Q900X3 polyomaviru
4	35	13.5	10	12	Q900X1 polyomaviru
5	35	13.5	10	12	Q900W9 polyomaviru
6	35	13.5	10	12	Q900W7 polyomaviru
7	35	13.5	10	12	Q900W5 polyomaviru
8	35	13.5	10	12	Q900W3 polyomaviru
9	35	13.5	10	12	Q900W1 polyomaviru
10	35	13.5	10	12	Q900V9 polyomaviru
11	35	13.5	10	12	Q900V7 polyomaviru
12	33.5	12.9	24	2	Q9f7T8 polyomaviru
13	33	12.7	15	4	Q9UBW5 chlamydia t
14	32	12.3	20	8	Q9ubm5 homo sapien
15	32	12.3	20	13	Q36584 nicotiana g
16	32	12.3	21	4	Q9PS63 gallus galli
					075073 homo sapien

17	31.5	12.1	27	2	Q48982 mycoplasma
18	31	11.9	11	5	Q26092 plisaster oc
19	31	11.9	12	10	Q93YC8 nicotiana t
20	31	11.9	19	15	Q905G4 human immun
21	31	11.9	20	2	Q9RAD7 escherichia
22	31	11.9	21	10	Q9M3S8 arabidopsis
23	31	11.9	25	2	Q9RAC8 mycoplasma
24	31	11.9	25	5	Q94683 polyandroca
25	31	11.9	26	10	Q94195 atropa bell
26	30	11.5	15	4	Q9BXX4 homo sapien
27	30	11.5	17	4	Q9UCN0 homo sapien
28	30	11.5	18	4	Q9UCT9 homo sapien
29	30	11.5	20	6	Q9TRW4 bos taurus
30	30	11.5	21	2	Q9SLC0 porphyromon
31	30	11.5	23	2	P71216 escherichia
32	30	11.5	26	12	Q69098 herpes simp
33	30	11.5	27	6	Q9TRW3 bos taurus
34	30	11.5	27	6	Q9TR26 bos taurus
35	30	11.5	27	10	Q9S8M0 solanum tub
36	30	11.5	27	12	O56464 hepatitis c
37	30	11.5	27	12	O56465 hepatitis c
38	30	11.5	27	12	O56469 hepatitis c
39	30	11.5	27	12	O56470 hepatitis c
40	30	11.5	27	12	O56494 hepatitis c
41	30	11.5	27	12	O56496 hepatitis c
42	30	11.5	27	12	O56507 hepatitis c
43	30	11.5	27	12	O56509 hepatitis c
44	30	11.5	27	12	O56551 hepatitis c
45	30	11.5	27	12	Q9QRS2 hepatitis c

ALIGNMENTS

RESULT 1

Q900X9 PRELIMINARY; PRT; 10 AA.
 AC Q900X9;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE LARGE T ANTIGEN (FRAGMENT).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCNU;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL: AF119345; AAF24096.1;
 FT NON TER
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 13.5%; Score 35; DB 12; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 36 PRTPPP 41

Db 4 PKTPPP 9

RESULT 2

Q900X5 PRELIMINARY; PRT; 10 AA.
 ID Q900X5;
 AC Q900X5;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DE 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE LARGE T ANTIGEN (FRAGMENT).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCN16;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119347; AAF24100.1; -;
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 13.5%; Score 35; DB 12; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 36 PRTPPP 41
 Db 4 PKTPPP 9

RESULT 3

OY00X3 PRELIMINARY; PRT; 10 AA.
 AC OY00X3;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE LARGE T ANTIGEN (FRAGMENT).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BCN8;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119348; AAF24102.1; -;
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 13.5%; Score 35; DB 12; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 36 PRTPPP 41
 Db 4 PKTPPP 9

RESULT 4

OY00X1 PRELIMINARY; PRT; 10 AA.
 AC OY00X1;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE LARGE T ANTIGEN (FRAGMENT).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=BCN15;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119349; AAF24104.1; -;
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;
 Query Match 13.5%; Score 35; DB 12; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 36 PRTPPP 41
 Db 4 PKTPPP 9

RESULT 5

OY00W9 PRELIMINARY; PRT; 10 AA.
 AC OY00W9;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE LARGE T ANTIGEN (FRAGMENT).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UNE3;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119350; AAF24106.1; -;
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 13.5%; Score 35; DB 12; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 36 PRTPPP 41
 Db 4 PKTPPP 9

RESULT 6

OY00W7 PRELIMINARY; PRT; 10 AA.
 AC OY00W7;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE LARGE T ANTIGEN (FRAGMENT).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NANCY2;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119351; AAF24108.1; -;

FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 13.5%; Score 35; DB 12; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 36 PRTPPP 41
Db 4 PKTPPP 9

RESULT 7

Q9Q0W5 PRELIMINARY; PRT; 10 AA.
AC Q9Q0W5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE LARGE T ANTIGEN (FRAGMENT).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRETORIA3;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119352; AAF24110.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 13.5%; Score 35; DB 12; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 36 PRTPPP 41
Db 4 PKTPPP 9

RESULT 8

Q9Q0W3 PRELIMINARY; PRT; 10 AA.
AC Q9Q0W3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE LARGE T ANTIGEN (FRAGMENT).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRETORIA1;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119353; AAF24112.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 13.5%; Score 35; DB 12; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 36 PRTPPP 41
Db 4 PKTPPP 9

RESULT 9

Q9Q0W1 PRELIMINARY; PRT; 10 AA.
AC Q9Q0W1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE LARGE T ANTIGEN (FRAGMENT).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFB;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119354; AAF24114.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 13.5%; Score 35; DB 12; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 36 PRTPPP 41
Db 4 PKTPPP 9

RESULT 10

Q9Q0V9 PRELIMINARY; PRT; 10 AA.
AC Q9Q0V9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE LARGE T ANTIGEN (FRAGMENT).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSFB;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119355; AAF24116.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 13.5%; Score 35; DB 12; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 36 PRTPPP 41
Db 4 PKTPPP 9

RESULT 11

Q900V7

ID Q900V7 PRELIMINARY; PRT; 10 AA.
 AC Q900V7;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DE LARGE T ANTIGEN (FRAGMENT).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CSFJ;
 RX MEDLINE=20087544; PubMed=10618230;
 RA Bofill-Mas S., Pina S., Girones R.;
 RT "Documenting the epidemiologic patterns of polyomaviruses in human
 populations by studying their presence in urban sewage.";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL; AF119356; AAF24118.1; -;
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 13.5%; Score 35; DB 12; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 36 PRTPPP 41

|:||||

Db 4 PKTPPP 9

RESULT 12

Q9F7T8 PRELIMINARY; PRT; 24 AA.
 ID Q9F7T8;
 DT 01-MAR-2001 (TEMBLrel. 16, Created)
 DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE TRUNCATED INCLUSION MEMBRANE PROTEIN A.
 GN INCA.
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MT1129;
 RA Viratyosin W., Rockey D.D., Suchland R.J., Stamm W.E.;
 RT "Diverse Mutations in Inca Amplified from Clinical Chlamydia
 trachomatis Isolates that occupy Nonfusogenic Inclusions.";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF276501; AAG22497.1; -;
 SQ SEQUENCE 24 AA; 2495 MW; B4A617A7369894AD CRC64;

Query Match 12.9%; Score 33.5; DB 2; Length 24;
 Best Local Similarity 72.7%; Pred. No. 1.1e+03;
 Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 33 IVTPPTPP-PS 42

||||:||||

Db 7 IVTPPPPPPS 17

RESULT 13

Q9UBM5 PRELIMINARY; PRT; 15 AA.
 ID Q9UBM5;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
 DE TUMOR NECROSIS FACTOR ALPHA (FRAGMENT).
 GN TNFA OR TNF-ALPHA.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RA Schagdarsurengin U., Glaeser C.;
 RT "Polymorphism in intron 3 of TNFA: transition A to G.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RA Schagdarsurengin U., Glaeser C.;
 RT "Amino acid substitution Pro to Leu in exon 3 on position +84 of TNF
 alpha.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ270944; CAB65595.1; -;
 DR EMBL; AJ251878; CAB63904.1; -;
 DR EMBL; AJ251879; CAB63905.1; -;
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1567 MW; 804891AE1E4EFAE5 CRC64;

Query Match 12.7%; Score 33; DB 4; Length 15;
 Best Local Similarity 46.2%; Pred. No. 7.5e+02;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 16 SHGRTQDENPVVH 28

|:||||

Db 1 SSSRTFSDKPVVH 13

RESULT 14

Q36584 PRELIMINARY; PRT; 20 AA.
 ID Q36584;
 AC Q36584;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE RPS19', PROTEIN (FRAGMENT).
 GN RPS19'.
 OS Nicotiana glauca (Glaucaus tobacco) (Tree tobacco).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UNIV. OF BIRMINGHAM, SOLANACEAE SEED COLLECTION, # BIRM S.0024;
 RX MEDLINE=96397499; PubMed=8804393;
 RA Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
 RT "Ebb and Flow of the Chloroplast Inverted Repeat.";
 RL Mol. Gen. Genet. 252:195-206(1996).
 DR EMBL; Z71244; CAA94954.1; -;
 DR InterPro; IPR002222; Ribosomal_S19.
 DR Pfam; PF00203; Ribosomal_S19; 1.
 KW Chloroplast.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 2388 MW; 2FC9AA300459DELD CRC64;

Query Match 12.3%; Score 32; DB 8; Length 20;
 Best Local Similarity 47.1%; Pred. No. 1.4e+03;
 Matches 8; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

Qy 19 RTQDENPVV--HFEKNI 33

|:||||

Db 3 RSLKKNPFVANHLPKKI 19

D	Q93YC8	PRELIMINARY;	PRT;
C	Q93YC8:		
V	01-DEC-2001	(TrEMBLrel. 19, Created)	
T	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
T	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
E		FUTATIVE COAT PROTEIN (FRAGMENT).	

AC	Q9R4D7:
DT	01-MAY-2000 (TREMBlrel. 13, Created)
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)

RESULT	23	
Q9R4C8		
ID	Q9R4C8	
AC	Q9R4C8	PRELIMINARY; PRT; 25 AA.
DT	01-MAY-2000	{TEMBRel. 13, Created}
DT	01-MAY-2000	{TEMBRel. 13, Last sequence update}
DT	01-MAY-2000	{TEMBRel. 13, Last annotation update}
DE	48 KDA OUTER MEMBRANE PROTEIN (FRAGMENT).	
OS	Mycoplasma hyopneumoniae.	
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; M	

OC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2099;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=96276661; PubMed=8673256;
 RA Lee R.P., Doughty S.W., Ashman K., Walker J.;
 RT "Purification of hydrophobic integral membrane proteins from
 RT Mycoplasma hyopneumoniae by reversed-phase high-performance liquid
 RT chromatography";
 RL J. Chromatogr. A 737:273-279(1996).
 SQ SEQUENCE 25 AA; 2566 MW; 19D50E895E6B3DA0 CRC64;

Query Match 11.9%; Score 31; DB 2; Length 25;
 Best Local Similarity 50.0%; Pred. No. 2.5e+03;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 14 OKSHGRTQDENP 25
 I : : I I I I I
 Db 5 QTESGSTNDEKP 16

RESULT 24

Q94683 ID Q94683 PRELIMINARY; PRT; 25 AA.
 AC Q94683;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PMNXX (FRAGMENT).
 OS Polyandrocarpa misakiensis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Styelidae; Polyandrocarpa.
 OX NCBI_TaxID=7723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USHIMADO;
 RA Fujiwara S., Kawamura K.;
 RT "Cloning of homeobox-containing genes from the budding ascidian
 RT Polyandrocarpa misakiensis";
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D88276; BAA13572.1;
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox; 1.
 FT NON_TER 1
 FT 25
 SQ SEQUENCE 25 AA; 2884 MW; D012BEE718D93472 CRC64;

Query Match 11.9%; Score 31; DB 5; Length 25;
 Best Local Similarity 38.5%; Pred. No. 2.5e+03;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 RTAHYGLPKSH 17
 I : : I I I I I
 Db 1 QTTRYLSAPERH 13

RESULT 25

Q94195 ID Q94195 PRELIMINARY; PRT; 26 AA.
 AC Q94195;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PUTATIVE ATP2 PROTEIN (FRAGMENT).
 OS Atropa belladonna (Belladonna).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Atropa.
 OX NCBI_TaxID=33113;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Nouar E., Baucher M., Jaziri M.;
 RT "Differential gene expression in Atropa belladonna leafy gall";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RA Nouar E.;
 RL Thesis (2001), Department of Plant Biotechnology,
 RL Université Libre de Bruxelles, Brussels, Belgium.
 DR EMBL: AJ309377; CAC40747.1;
 FT NON_TER 1
 FT 1
 SQ SEQUENCE 26 AA; 2820 MW; 7A41A9C31E93EAE4 CRC64;

Query Match 11.9%; Score 31; DB 10; Length 26;
 Best Local Similarity 35.0%; Pred. No. 2.6e+03;
 Matches 7; Conservative 3; Mismatches 6; Indels 4; Gaps 1;

QY 6 TAYHGLPKSHGRTQDENP 25
 I : : I I I I I
 Db 5 TTYFNAPQ----MFSDENP 20

RESULT 26

Q9EXX4 ID Q9EXX4 PRELIMINARY; PRT; 15 AA.
 AC Q9EXX4;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TRANSCRIPTION FACTOR PAX 5 (PAX5) (FRAGMENT).
 GN PAX5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hirabayashi Y., Rahman M., Sasaki T.;
 RT "Identification of a novel repressor element in the 5'UTR of human
 RT BSP/Pax5A";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21354098; PubMed=11460166;
 RA Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
 RA Chaganti R.S.K., Kuppers R., Dalla-Pavera R.;
 RT "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
 RT cell lymphomas";
 RL Nature 412:341-346(2001).
 DR EMBL: AF268279; AAK25737.1;
 DR EMBL: AF386790; AAK70869.1;
 FT NON_TER 15
 FT 15
 SQ SEQUENCE 15 AA; 1809 MW; 3F95BB53FB3F7A8E CRC64;

Query Match 11.5%; Score 30; DB 4; Length 15;
 Best Local Similarity 75.0%; Pred. No. 1.9e+03;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 31 KNIVTPRT 38
 I : : I I I I I
 Db 5 KNYTPRT 12

RESULT 27

Q9UCNO ID Q9UCNO PRELIMINARY; PRT; 17 AA.
 AC Q9UCNO;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE TRANSFERRIN RECEPTOR.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92375195; PubMed=1380674;
 RA Chicx R.M., Urban R.G., Lane W.S., Gorga J.C., Stern L.J.,
 RA Vignall D.A., Strominger J.L.;
 RT "Predominant naturally processed peptides bound to HLA-DRI are derived
 from MHC-related molecules and are heterogeneous in size.";
 RL Nature 358:764-768(1992).
 SQ SEQUENCE 17 AA; 2035 MW; A7DEDA39A2538A88 CRC64;

Query Match 11.5%; Score 30; DB 4; Length 17;
 Best Local Similarity 38.5%; Pred. No. 2.2e+03;
 Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 28 HFEKNIVTPRPP 40
 II I I I
 Db 5 HFLSPYVSPKSP 17

RESULT 28
 ID Q9UCT9 PRELIMINARY; PRT; 18 AA.
 AC Q9UCT9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE PRG-PROLINE-RICH GLYCOPROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91373355; PubMed=1894623;
 RA Gillete-Castro B.L., Prakhophol A., Burlingame A.L., Leffler H.,
 RA Fisher S.J.;
 RT "Structure and bacterial receptor activity of a human salivary
 proline-rich glycoprotein.";
 RL J. Biol. Chem. 266:17358-17368(1991).
 SQ SEQUENCE 18 AA; 1780 MW; 961F6FB0A83D2E40 CRC64;

Query Match 11.5%; Score 30; DB 4; Length 18;
 Best Local Similarity 71.4%; Pred. No. 2.3e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 39 PPPSQGK 45
 III I I
 Db 4 PPPRFGK 10

RESULT 29
 ID Q9TRW4 PRELIMINARY; PRT; 20 AA.
 AC Q9TRW4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE 25 KDA PROTEIN P25, PEPTIDE F5A.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91372400; PubMed=1909972;
 RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
 RA Shiratsuchi A., Uchida T., Imahori K.;

RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
 Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";
 RL FEBS Lett. 289:37-43(1991).
 SQ SEQUENCE 20 AA; 2032 MW; 4AADB849A6416897 CRC64;

Query Match 11.5%; Score 30; DB 6; Length 20;
 Best Local Similarity 55.6%; Pred. No. 2.6e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 37 RTPPPSQK 45
 : I I I I I
 Db 4 KTPPKSPGE 12

RESULT 30
 ID Q9SIC0 PRELIMINARY; PRT; 21 AA.
 AC Q9SIC0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE TRANSPOSASE (FRAGMENT).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; CF group; Bacteroidetes; Bacteroidales; Porphyromonadaceae;
 OC Porphyromonas.
 OX NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W83;
 RX MEDLINE=20002534; PubMed=10531208;
 RA Sawada K., Kokeguchi S., Hongyo H., Sawada S., Miyamoto M., Maeda H.,
 RA Nishimura F., Takashiba S., Murayama Y.;
 RT "Identification by subtractive hybridization of a novel insertion
 sequence specific for virulent strains of Porphyromonas gingivalis.";
 RL Infect. Immun. 67:5621-5625(1999).
 DR EMBL; AB011547; BAA83478.1;
 FT NON-TER 1
 SQ SEQUENCE 21 AA; 2543 MW; 08D3F838FB3E6AF CRC64;

Query Match 11.5%; Score 30; DB 2; Length 21;
 Best Local Similarity 83.3%; Pred. No. 2.8e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 PRTPPP 41
 I I I I I
 Db 9 PFTPPP 14

RESULT 31
 ID P71216 PRELIMINARY; PRT; 23 AA.
 AC P71216;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE FAE (FRAGMENT).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86176742; PubMed=2870470;
 RA Mooli F.R., Claassen I., Bakker D., Kuipers H., de Graaf F.K.;
 RT "Regulation and structure of an Escherichia coli gene coding for an
 outer membrane protein involved in export of K88ab fimbrial
 subunits.";
 RL Nucleic Acids Res. 14:2443-2457(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Oudega B.;

RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X03675; CA227311.1; -.
 FT NON_TER 23
 SQ SEQUENCE 23 AA; 2588 MW; D5FF3BEA22462544 CRC64;

Query Match 11.5%; Score 30; DB 2; Length 23;
 Best Local Similarity 58.3%; Pred. No. 3e+03;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 24 NPVVHFFKNIVT 35
 Db 5 NAVTFTINRVT 16

RESULT 32
 Q69098 PRELIMINARY; PRT; 26 AA.

AC Q69098;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE VIRION PROTEIN 19C (FRAGMENT).
 OS Herpes simplex virus (type 2).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=10310;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90156509; PubMed=2154597;
 RA Yel S., Chowdhury S.I., Bhat B.M., Conley A.J., Wold W.S.,
 RA Batterson W.;
 RT "Identification and characterization of the Herpes simplex virus type
 RT 2 gene encoding the essential capsid protein ICP32/Vp19c.";
 RL J. Virol. 64:1124-1134(1990).
 DR EMBL; M33905; AAA45845.2; -.
 FT NON_TER 26
 SQ SEQUENCE 26 AA; 2501 MW; D9B9FE63E374922A CRC64;

Query Match 11.5%; Score 30; DB 12; Length 26;
 Best Local Similarity 45.5%; Pred. No. 3.5e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 34 VTPRTPPPSQ 44
 Db 14 MTPPSAPPNG 24

RESULT 33
 Q9TRW3 PRELIMINARY; PRT; 27 AA.

AC Q9TRW3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE 25 KDA PROTEIN P25, PEPTIDE F5B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91372400; PubMed=1909972;
 RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
 RA Shiratsuchi A., Uchida T., Imahori K.;
 RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
 RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";
 RL FEBS Lett. 289:37-43(1991).
 SQ SEQUENCE 27 AA; 2787 MW; 8DCFE1D811407B23 CRC64;

Query Match 11.5%; Score 30; DB 6; Length 27;
 Best Local Similarity 55.6%; Pred. No. 3.7e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 37 RTPPPSQGK 45
 Db 11 KTPPKSPGE 19

RESULT 34
 Q9TR26 PRELIMINARY; PRT; 27 AA.

AC Q9TR26;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE PIGMENT EPITHELIUM-DERIVED FACTOR (FRAGMENT).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96136631; PubMed=8527930;
 RA Wu Y.Q., Notario V., Chader G.J., Becerra S.P.;
 RT "Identification of pigment epithelium-derived factor in the
 RT interphotoreceptor matrix of bovine eyes.";
 RL Protein Expr. Purif. 6:447-456(1995).
 SQ SEQUENCE 27 AA; 2845 MW; 5440D85FB485F2E1 CRC64;

Query Match 11.5%; Score 30; DB 6; Length 27;
 Best Local Similarity 39.1%; Pred. No. 3.7e+03;
 Matches 9; Conservative 5; Mismatches 5; Indels 4; Gaps 2;

Qy 10 GSLPKOKSHGR-TODENPVVHFFK 31
 Db 7 GSLTPESXGAPVEEDP---FFR 26

RESULT 35
 Q9S8M0 PRELIMINARY; PRT; 27 AA.

AC Q9S8M0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE LECTIN-CHIITIN-BINDING PROTEIN.
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94333159; PubMed=8054990;
 RA Kieliszewski M.J., Showalter A.M., Leykam J.F.;
 RT "Potato lectin: a modular protein sharing sequence similarities with
 RT the extensin family, the hevein lectin family, and snake venom
 RT disintegrins (platelet aggregation inhibitors).";
 RL Plant J. 5:849-861(1994).
 DR InterPro: IPR002965; P-rich extensin.
 DR PRINTS: PR01217; PRICEXTENSIN.
 SQ SEQUENCE 27 AA; 2646 MW; 53916129AE222223 CRC64;

Query Match 11.5%; Score 30; DB 10; Length 27;
 Best Local Similarity 71.4%; Pred. No. 3.7e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 36 PRTPPPS 42
 Db 11

Db 11 PSPPPPS 17

RESULT 36

O56464

ID O56464 PRELIMINARY; PRT; 27 AA.

AC O56464;

DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70) (NS1)] (FRAGMENT).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Hepacivirus.

OX NCBI_TaxID=11103;

RN [1]

RP SEQUENCE FROM N.A.

RA Pan W.S., Wang H.T., Guo H.Z., Wang T.;

RT "Complete hypervariable region gene of hepatitis C virus from plasma 1991 of patient No.29-1.";

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF040790; AAB95515.1; -.

DR InterPro: IPR002531; HCV_NSI.

DR Pfam: PF01560; HCV_NSI; 1.

KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;

KW Polyprotein; Transmembrane.

FT NON_TER 1

FT NON_TER 27

FT NON_TER 27

SQ SEQUENCE 27 AA; 2718 MW; B129AEA218640FC9 CRC64;

Query Match 11.5%; Score 30; DB 12; Length 27;

Best Local Similarity 43.8%; Pred. No. 3.7e+03;

Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 28 HFFKNIVTPRTPPSQ 43

Db 11 HTTSRIVSLSPGPSQ 26

RESULT 37

O56465

ID O56465 PRELIMINARY; PRT; 27 AA.

AC O56465;

DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70) (NS1)] (FRAGMENT).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Hepacivirus.

OX NCBI_TaxID=11103;

RN [1]

RP SEQUENCE FROM N.A.

RA Pan W.S., Wang H.T., Guo H.Z., Wang T.;

RT "Complete hypervariable region gene of hepatitis C virus from plasma 1991 of patient No.29-1.";

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF040792; AAB95517.1; -.

DR InterPro: IPR002531; HCV_NSI.

DR Pfam: PF01560; HCV_NSI; 1.

KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;

KW Polyprotein; Transmembrane.

FT NON_TER 1

FT NON_TER 27

FT NON_TER 27

SQ SEQUENCE 27 AA; 2718 MW; B129AEA218640FC9 CRC64;

Query Match 11.5%; Score 30; DB 12; Length 27;

Best Local Similarity 43.8%; Pred. No. 3.7e+03;

Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 28 HFFKNIVTPRTPPSQ 43

Db 11 HTTSRIVSLSPGPSQ 26

OY 28 HFFKNIVTPRTPPSQ 43

Db 11 HTTSRIVSLSPGPSQ 26

RESULT 38

O56469

ID O56469 PRELIMINARY; PRT; 27 AA.

AC O56469;

DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70) (NS1)] (FRAGMENT).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Hepacivirus.

OX NCBI_TaxID=11103;

RN [1]

RP SEQUENCE FROM N.A.

RA Pan W.S., Wang H.T., Guo H.Z., Wang T.;

RT "Complete hypervariable region gene of hepatitis C virus from plasma 1994 of patient No.29-1.";

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF040796; AAB95521.1; -.

DR InterPro: IPR002531; HCV_NSI.

DR Pfam: PF01560; HCV_NSI; 1.

KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;

KW Polyprotein; Transmembrane.

FT NON_TER 1

FT NON_TER 27

FT NON_TER 27

SQ SEQUENCE 27 AA; 2718 MW; B129AEA218640FC9 CRC64;

Query Match 11.5%; Score 30; DB 12; Length 27;

Best Local Similarity 43.8%; Pred. No. 3.7e+03;

Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 28 HFFKNIVTPRTPPSQ 43

Db 11 HTTSRIVSLSPGPSQ 26

RESULT 39

O56470

ID O56470 PRELIMINARY; PRT; 27 AA.

AC O56470;

DT 01-JUN-1998 (TREMBlrel. 06, Created)

DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70) (NS1)] (FRAGMENT).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Hepacivirus.

OX NCBI_TaxID=11103;

RN [1]

RP SEQUENCE FROM N.A.

RA Pan W.S., Wang H.T., Guo H.Z., Wang T.;

RT "Complete hypervariable region gene of hepatitis C virus from plasma 1994 of patient No.29-1.";

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF040797; AAB95522.1; -.

DR InterPro: IPR002531; HCV_NSI.

DR Pfam: PF01560; HCV_NSI; 1.

KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;

KW Polyprotein; Transmembrane.

FT NON_TER 1

FT NON_TER 27

FT NON_TER 27

SQ SEQUENCE 27 AA; 2744 MW; B129AEA2186419A5 CRC64;

Query Match 11.5%; Score 30; DB 12; Length 27;
 Best Local Similarity 43.8%; Pred. No. 3.7e+03;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 28 HFEKNIVTPRTPPSQ 43
 I II: :I I I I
 Db 11 HTTSRIVSILSPGPSQ 26

RESULT 40
 O56494 PRELIMINARY; PRT; 27 AA.
 ID O56494;
 AC O56494;
 DT 01-JUN-1998 (TREMELREL. 06, Created)
 DT 01-JUN-1998 (TREMELREL. 06, Last sequence update)
 DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
 DE (NSI)] (FRAGMENT).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pan W.S., Wang H.T., Guo H.Z., Wang T.;
 RT "Complete hypervariable region gene of hepatitis C virus from plasma
 RT 1996 of patient No.29-1.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF040823; AAB95548.1; -;
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01560; HCV_NSI; 1.
 DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 27 27
 SQ SEQUENCE 27 AA; 2718 MW; B129AEA218640FC9 CRC64;

Query Match 11.5%; Score 30; DB 12; Length 27;
 Best Local Similarity 43.8%; Pred. No. 3.7e+03;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 28 HFEKNIVTPRTPPSQ 43
 I II: :I I I I
 Db 11 HTTSRIVSILSPGPSQ 26

RESULT 41
 O56496 PRELIMINARY; PRT; 27 AA.
 ID O56496;
 AC O56496;
 DT 01-JUN-1998 (TREMELREL. 06, Created)
 DT 01-JUN-1998 (TREMELREL. 06, Last sequence update)
 DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
 DE (NSI)] (FRAGMENT).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pan W.S., Wang H.T., Guo H.Z., Wang T.;
 RT "Complete hypervariable region gene of hepatitis C virus from plasma
 RT 1996 of patient No.29-1.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF040825; AAB95550.1; -;
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01560; HCV_NSI; 1.
 DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 27 27

Query Match 11.5%; Score 30; DB 12; Length 27;
 Best Local Similarity 43.8%; Pred. No. 3.7e+03;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 28 HFEKNIVTPRTPPSQ 43
 I II: :I I I I
 Db 11 HTTSRIVSILSPGPSQ 26

RESULT 42
 O56507 PRELIMINARY; PRT; 27 AA.
 ID O56507;
 AC O56507;
 DT 01-JUN-1998 (TREMELREL. 06, Created)
 DT 01-JUN-1998 (TREMELREL. 06, Last sequence update)
 DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
 DE (NSI)] (FRAGMENT).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pan W.S., Wang H.T., Guo H.Z., Wang T.;
 RT "Complete hypervariable region gene of hepatitis C virus from plasma
 RT 1996 of patient No.29-1.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF040823; AAB95548.1; -;
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01560; HCV_NSI; 1.
 DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 27 27
 SQ SEQUENCE 27 AA; 2718 MW; B129AEA218640FC9 CRC64;

Query Match 11.5%; Score 30; DB 12; Length 27;
 Best Local Similarity 43.8%; Pred. No. 3.7e+03;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 28 HFEKNIVTPRTPPSQ 43
 I II: :I I I I
 Db 11 HTTSRIVSILSPGPSQ 26

RESULT 43
 O56509 PRELIMINARY; PRT; 27 AA.
 ID O56509;
 AC O56509;
 DT 01-JUN-1998 (TREMELREL. 06, Created)
 DT 01-JUN-1998 (TREMELREL. 06, Last sequence update)
 DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
 DE (NSI)] (FRAGMENT).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pan W.S., Wang H.T., Guo H.Z., Wang T.;
 RT "Complete hypervariable region gene of hepatitis C virus from plasma
 RT 1996 of patient No.29-1.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF040825; AAB95550.1; -;
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01560; HCV_NSI; 1.
 DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 27 27

QY 28 HFEKNIVTPRTPPSQ 43
 I II: :I I I I
 Db 11 HTTSRIVSILSPGPSQ 26

RESULT 42
 O56507 PRELIMINARY; PRT; 27 AA.
 ID O56507;
 AC O56507;
 DT 01-JUN-1998 (TREMELREL. 06, Created)
 DT 01-JUN-1998 (TREMELREL. 06, Last sequence update)
 DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
 DE (NSI)] (FRAGMENT).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pan W.S., Wang H.T., Guo H.Z., Wang T.;
 RT "Complete hypervariable region gene of hepatitis C virus from plasma
 RT 1996 of patient No.68-1.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF040837; AAB95562.1; -;
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01560; HCV_NSI; 1.
 DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polyprotein; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 27 27
 SQ SEQUENCE 27 AA; 2719 MW; B129AA02B2640FC9 CRC64;

Query Match 11.5%; Score 30; DB 12; Length 27;
 Best Local Similarity 43.8%; Pred. No. 3.7e+03;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 28 HFEKNIVTPRTPPSQ 43
 I II: :I I I I
 Db 11 HTTSRIVSILSPGPSQ 26

RESULT 43
 O56509 PRELIMINARY; PRT; 27 AA.
 ID O56509;
 AC O56509;
 DT 01-JUN-1998 (TREMELREL. 06, Created)
 DT 01-JUN-1998 (TREMELREL. 06, Last sequence update)
 DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70)
 DE (NSI)] (FRAGMENT).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pan W.S., Wang H.T., Guo H.Z., Wang T.;
 RT "Complete hypervariable region gene of hepatitis C virus from plasma
 RT 1996 of patient No.68-1.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF040839; AAB95564.1; -;
 DR InterPro; IPR002531; HCV_NSI.
 DR Pfam; PF01560; HCV_NSI; 1.
 DR Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;

KW Polyprotein; Transmembrane.
 FT NON_TER 1
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2718 MW; B129AEA218640FC9 CRC64;

Query Match 11.5%; Score 30; DB 12; Length 27;
 Best Local Similarity 43.8%; Pred. No. 3.7e+03;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 28 HFFKNIVTPTPTPPSQ 43
 DB 11 HTTSRIVSILSPGPSQ 26

RESULT 44

O56551 ID O56551 PRELIMINARY; PRT; 27 AA.
 AC O56551;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70) (NS1)] (FRAGMENT).
 DE Hepatitis C virus.
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OC NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pan W.S., Wang H.T., Guo H.Z., Wang T.;
 RT "Hypervariable region gene sequences of Hepatitis C virus."; Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF040881; AAB95606.1; -.
 DR InterPro; IPR002531; HCV_NSL.
 DR Pfam: PF01560; HCV_NSL; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
 FT NON_TER 1
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2718 MW; B129AEA218640FC9 CRC64;

Query Match 11.5%; Score 30; DB 12; Length 27;
 Best Local Similarity 43.8%; Pred. No. 3.7e+03;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 28 HFFKNIVTPTPTPPSQ 43
 DB 11 HTTSRIVSILSPGPSQ 26

RESULT 45

O9QRS2 ID O9QRS2 PRELIMINARY; PRT; 27 AA.
 AC O9QRS2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE GENOME POLYPROTEIN [CONTAINS: ENVELOPE GLYCOPROTEIN E2 (GP68) (GP70) (NS1)] (FRAGMENT).
 DE Hepatitis C virus.
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OC NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DS;
 RA Yeh C.-I.;
 RT "Hepatitis C virus hypervariable regions in patients with liver cirrhosis."; Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF110014; AAD49801.1; -.

DR InterPro; IPR002531; HCV_NSL.
 DR Pfam: PF01560; HCV_NSL; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
 FT NON_TER 1
 FT NON_TER 27
 SQ SEQUENCE 27 AA; 2795 MW; 204C686C97D415EE CRC64;

Query Match 11.5%; Score 30; DB 12; Length 27;
 Best Local Similarity 33.3%; Pred. No. 3.7e+03;
 Matches 6; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 26 VVHFFKNIVTPTPTPPSQ 43
 DB 9 VAHTISRVTSLFSPGPSQ 26

Search completed: September 23, 2002, 11:10:50
 Job time: 114 sec